

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 105371

TO: Rebecca Prouty

Location: CM1/10A13/10D01

Art Unit: 1652

Friday, October 10, 2003

Case Serial Number: 09/884889

From: Edward Hart

**Location: Biotech-Chem Library** 

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

#### Search Notes

Examiner Prouty,

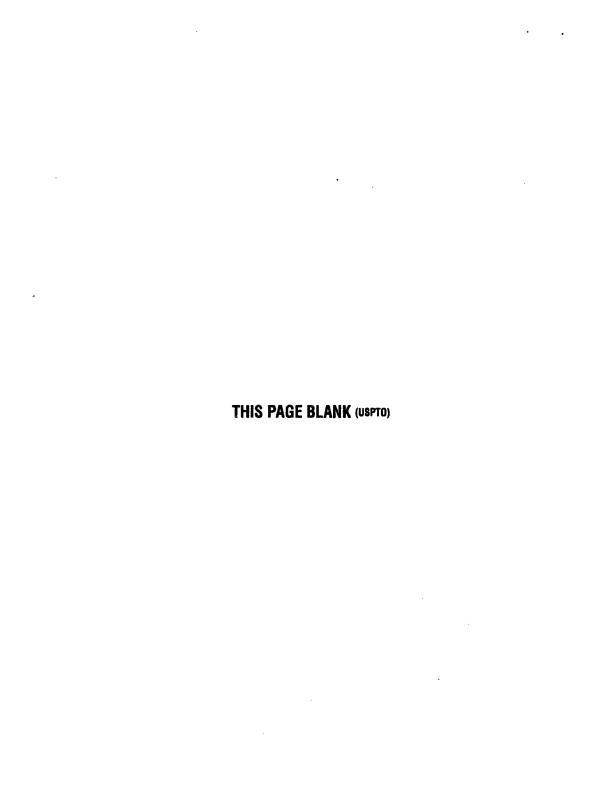
Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 

ar all others & comments





#### STIC-Biotech/ChemLib

From: Sent:

To:

Prouty, Rebecca Monday, October 06, 2003 8:48 AM STIC-Biotech/ChemLib

Subject:

Sequence Search

Art Unit 1652, 10A13 Mailbox: 10D01 308-4000

Serial Number: 09/884,889

Please search and interference search SEQ NOS: 5-8

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coward Hart Technical Info. Specialist STIC/Biotech ON 6802 Tel: 305-9203

Searcher:
Phone:
Location:
Date Picked Up: 10 11 10
Date Completed: 10/19/03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)	)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	_
Lexis/Nexis:	
Sequence Sys.: (VY.//)	QY
www/Internet: ' 7'	
Other (specify):	

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### STIC SEARCH RESULTS

### Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

VO.	luntary Results Feedback Form
A	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	□ Non-Patent Literature     (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention
Coi	mments:

-Droplon or send/completed forms to STIC/Blotech-Ghem\Library/GMI = Girc/Desk



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COUNTRY: US
COUNTRY: 9037
COMPUTER READABLE FORM:
MUDION TYPE: DISACETC
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TRACESTER: MINIOWASSS
SOFTWARE: FASTERD ANTA:
APPLICATION NUMBER: US/08/674,887A
FILING DATE: 03-UUL-1996
FRION REPLICATION DATE:
APPLICATION NUMBER:
                                              US-08-777-653-115

US-08-775-653-114

US-08-720-946-1145

US-08-720-946-1145

US-08-720-946-1147

US-08-720-946-1147

US-08-914-0205-4

US-08-914-0205-4

US-08-014-0205-4

US-09-014-0205-1

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Hatches 2262; Conservative 0; Mismeria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Robertoon, Dan E. APPLICANT: Sanyal Indept S. TITLE OF TINVENTION: CATALASES NUMBER OF SEQUENCES: GARESPORTES ADDRESSEE: Fish & Richardson is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
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TELECOMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-509
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
TOPOLOGY: linear MOLECULE TYPE: CDNA
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/cgn2_6/ptodata/2/ina/FB_COMB.seq:*
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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	y 301 ccgttgatgaccgatagccaagactggtggccccgtgactgggggcactactactg 360	y 361 AUGATOCCHAGGCATGGCACCTACCGTACCGTATGCTGATGGCCGTGGGGCC 420	421 GGTGGTACCGAAGCCAGCGCTTTGCACCTCGTCAACTCGTGGCCGAACGTCAGCTG	421	481 GATARAGGGGGCGTCTGGTGTGGGCGATCAAAAAATGAGGAAAATGAGTGGGGGAAAATGAGTGGGGGG	1	601 GGCTTCTCTTTCGGCCGGTCGATATTTGGGAACCGAAAAAGATATTACTGGGGTGAC 	661	721	181 AACGGCCACCCTGATCCGCTGAGAACCGCACAGGTACTTGAAACCTTGGCCCGTATG 840	941 GCGATGAACGACGAAAAACCGCAGCCCTCACAGCTGGCGGCCACACCGTCGGTAATTGT 900  841 GCGATGAACGACGAAAAAACGCGAGCCCTCACAGCTGGCGCCACACGTCGGTAATTGT 900  841 GCGATGAACGACGAAAAAACGCGAGCCCTCACAACTGCGCGCCACACGTCGGTAATTGT 900	991 CACGGTAATGCCATCTGCGTTAACCCCTGACCCAAAAGCCTCTGACGTTGAAAAC 960 901 CACGGTAATGCCAATGCCTTGCGTTAACCCCTGACCCCAAAACCTTGAACTTGAAAAC 960 901 CACGGTAATGCCATTACCCCTGACCCCTGACCCTTGAAAAAC 960	961 CAGGGCTTAGGTGGGGCAACCCCAACGGGAAGGCAAGCAA	1021 GGTATCGAAGGTGCTTGGACCACCACGAAATTCGATATGGGCTATTTCGACGT 1080	TO 1081 CTGTTCGGCTACAATTGGAACTGAAAAACTCGCCGCCCCCCCC	DD 1141 ATTGACATCAAAAGGAAAACAGGGTTGACGCAGCGACCCTCTATTCGCCACAC 1200 CT   111   11   11   11   11   11   11	QY 1201 CGGATCATGACGGATATGGGGATAAAGGTAAATCGGACTATCGGCTATCTGC 1260	09 1261 GAAAATTCATGGCCGATCCTGAGAAACTTCGGGAAGGCGTGGTTCAAG 1320  Db 1261 GAAAATTCATGGCCGATCCTGAGATACTTCCAAGAAACTTTCGGGAAGGCGTGTTCAAG 1320  Db 1261 GAAAAATTCATGGTGGCGATCCTGAGAAACTTTCGGGAAGGCGTGTTAAG 1320	Qy 1321 CYGACGCACGGGACCGGGAAATCACGTTACATCGGCCGGGAGTGCCGGGAGA 1380
2220   Db	<i>₹</i>	& 6 	- A	qa oo	40 ————————————————————————————————————	ζο qα	λο qα 	λ <sub>0</sub> α	9y	4a -	ko qa	ф qq	do do	40 03	ko 09	120	180	240	300
	2221 ACCANAGTGATGACGACGGTTGGACGTCGGTCGTA 2262 	a		APPLICANT: Robertson et al. TITLE OF INVENTION: Catalases NUMBER OF SEQUENCES: 8	CORRESPONDENCE ADDRESS: ADDRESSEB: CARELLA, BYRNE, BAIN, GILFILLAN, ANDRESSER: CARELLA, SYRNE, BAIN, GILFILLAN,	STREET: 6 BECKER FARM ROAD CITY: ROSELAND CITY: TREET: NEW TOAD	COUNTRY: USA COMPUTER READALLE PORM: MEDIUM TYPE: 3.5 INCH DISKEFTE		APPLICATION NUMBER: US/08/951,844 FILING DATE: CLASSIFCRION: 435 LIOR APPLICATION DATA:	APPLICATION NUMBER: U8/04/88/ FILIG DAMP 1996 ATTORNEY/AGENT INTORNATION: NAME: Charles J. Herron	RESISTANT AND WORDERN 20-7-11400-55 RESISTANCE FOOCKET NUMBER: 031400-55 TELECOMOUNT(CATA) TO NUMBER: 0314-1700	INPORMATION FOR SEQ. ID NO. 5: SEQUENCE CHARACTURE SEQ. SEQ. POR SEQ. ID NO. 5: SEQ. POR SEQ. EXPERIENTE: SEG. POR SEQ. EXPERIENTE: SEG. NOCLEOTIDES  LEMENTE: SEG. NOCLEOTIDES	; TYPE: NOLMET ACLD STRANDEDVESS: SINGLE TOPOLOGY: LINEAR NOLMETURE TYPE: Oligonucleotide	Ouery Match 100.0%; Score 2262; DB 3; Length 2262; BB Best Local Similarity 100.0%; Pred, No. 0; Matches 2262; Conservative 0; Mismatches 0; Indels 0; Gans	CTGACGATCTACACGGGGGGGGGGGGGGGGGGGGGGGGG		CITCLITOR ALLOCCHANGE AL MAGNOCHATARNOS MAGNARACIA ILARGOGGI INMATORI CITCLITOR ALLOCCHANGE AL MAGNACHAT CANACHATARNOS MAGNARACIA AL MAGNATAR CITCLITOR AL MAGNATAR CANACHATARNOS MAGNACHATARNOS MAGNACHA	CONTROL CONTRO	

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COMPUTER REALABLE FORM:
MEDIUM TYPE: Discrete
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows5
SOFTWARE: FastSEQ for Windows Version 2.0
                            Ish & Richardson P.C.
Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,347
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/674,887 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: INTO THE A NUMBER: 35.347
RETERRACE/DOCKER WHERE: 09.01
TELECOMMULECATION INVENTION:
TELECHONE: 612/678-5770
INFORMATION FOR SED IN NO: 5: SEQUENCE CERRACEFESTICS:
LEMETH: 250 base set in the strange of the str
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NAME: Haile, Ph.D., Lisa
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
                            ADDRESSEE: F1sh
STREET: 4225 Exe
                                                                              CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                 COUNTRY: US
                                                                                                                                                          92037
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Sequence 5, Application US/09412347
Patent No. 6401290
RENEAL INFORMATION:
PAPLICANT: Robertson, Dan E. APPLICANT: Sanyal, Indrajit
APPLICANT: Adhikari, Robert S.
TITLE OF INVENTION: CATALASES
NUMBER OF SEQUENCES: 8

US-09-412-347-5

us-09-884-889-5.rni

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CATGCAGGCAAGCAACCAACCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAA 1046
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                                                                                      AGCCCCTGACCCAAAAGCCTCTGACGTTGAAAACCAGGGCTTAGGTTGGGGCAACCCCAA
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                                                                                                                                                                                                                                                                                                                                                                               Length 2238;
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Pred. No. 3.7e-179;
0; Mismatches 808;
                                                              MAKE: Helle Ph. Lisa A.
REGISTRATION NUBBR: 39.347
REGISTRATION NUBBR: 39.347
REFERENCE/COCKET WUBBR: 09015/002001
TELECOWHUICATION INPORMATION:
TELECOWHUICATION NUBBR: 0.0015/002001
INFORMATION FOR 950 ID NO: 5.0000NC MARACIPERISTICS:
LENGTH: 2.238 base pairs
TYPE: NUCLEC and CLECLE A.
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                         Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.7%;
Best Local Similarity 59.5%;
Matches 1277; Conservative
                                                ATTORNEY/AGENT INFORMATION
PRIOR APPLICATION DATA:
              APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                            , LOCATION:
US-08-674-887A-7
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us-09-884-889-5.rni

09   1575 CGAGTGGCAACGACCCCGGCGAAAGTGCTCAG	09   1731   GETCCTCCTGAAAGCCGGGGGGGGCGCCCGGGAGGGCGCGCGC		097   1971   1971   1974   1974   1975   1975   1975   1971   1974   1975   1	Qy   2085 GACCGTGCCTGAAGTGGACCGCCTCGGGGTGGATGTTGGTTCCAACTGGCT 2144	SULT 7  OB 410-782-20  OB 410-782-20  SAGENER IN S. 56591  APPLICANT: COCKFILIT, FRANKLIN R.  APPLICANT: COCKFILIT, FRANKLIN R.  APPLICANT: Wilne, Bruce C.  APPLICANT: Wilne, Bruce C.  APPLICANT: Wilne, Bruce C.  APPLICANT: Wilne, Defection of Isoniasid Resistant S.	TITIE OF INVENTION: Of W. Tuberoulosis NUMBER OF SOURCES: 2 CORRESPONDENCE ADDRESS: 3 ADDRESSER: Schwegman, Lundberg & Woessner STREET: 3500 IDS Center CITY: Minneapolis Center CITY: Minneapolis Conter CITY: Minneapolis STATE: WSA ZIP: 55402 ZIP: 55402 COMPRES: IN PC Compatible OOMPRTER: IN PC COMpatible OOMPRTER: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
0y 510 CAAGAAGAACTACGGGAACAAAATCAGGTGGGCAACCTGATGATTCTGGCTGG	ACCUTANCECACCIONACCACACACACACACACACACACCACCCCCCCCCC	ACAGCAGGTACTTGAAACCTTCGCCCGTATGGCGATGACGACGAGAAAAACGCCGCCCCT	927 AGCCCTGAACCCAAAAGCCTCTGAGGTTGAAAACCAGGGCTTAGGTTGGGGCAACCCCAA 966	CCCACGAANTTCGATATGGGCTATTTCGACCTGCTGTTCGCCTACANTTGGGAACTGAACT	1104 ACCGGATGCACATGATCCCAGCAGTCCTCCATTANGCTCACTACGACCTGGC 1163 1227 GATAAAGGTAAAATCCGACCTATCGCGAAAAATCCACGGACCGATCCTGGC 1128 1124 GTTAAAGGTAAAATCCGACCTATCGGAAAAATTCTCGACGGACCGATCGAAACCCTGATTA 1223 1287 CTTCAAGAAAACTTCGGCAAAGGCGTGGTTCAACTGGAAGCCGTGATCA 1346 1124 GTTCAAGAAAACTTTCGGCAAAGACCGTGATCAACTGAACTGAACTTTCGGCAAAACCTTAAACTTTCGGCAAAGACCGTGATCAATTTCGGAAAGACCGAAACTGAAACTGAAAACCTTAAATTTCGGAAAAACCGTAAACTAAAACCTGAAAACCGAAAACCGCGAAAAACCGAAAACCGAAAACCGAATTCC 1466 1347 ATCAACGTTAAAACCGCGCGCAAAAGACCGAAAACCGCAAAACCGCAATTCC 1466	GGTGGGCTACCTGGGACCAGAAGTGCCTCAGGAGACCTCATCGGCAAGACCCTATACC GGAGGTAACCTGGGACCAGAAGTGCCTCAGGAGACCTCATCGGCAAGACCCTATACC GCAGGTAACCTGCGAAAACCTACTGGGAGACCTCATCGGCAAGACCCTATACC GCAGGTAACCTTGTAAGACCAAAACGTTTGAAGGCCTAAAACCCTAAATCCT ACAAGTGGCGCGATCCTTGCAAGATGCTTCCACCTTGGAGCCAAAAACCCTACTTTGTAAGCCAAAAACCTACTACTACTACAAAACCTACTACTACAAAACCTACTA

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APPLICATION NUMBER: US/08/418,782
PILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WOGSIGE, WATERD D.
REGISTRATION UNMBER: 30,440
REFERENCE/COCKET NUMBER: 30,440
REFERENCE/COCKET NUMBER: 30,440
REFERENCE/COCKET NUMBER: 30,440
REPERENCE/COCKET NUMBER: 30,440
RELEMONICATION INFORMATION:
TELECHONICATION INFORMATION:
TELECHONICATION TO SECURICATION:
TELECHONICATION TO SECURICATION 
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Best Local Similarity 58
Matches 1253; Conservativ
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592 TCGATGGGCTTCAA
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814 CGCGAGACGTTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
; LOCATION: 70..2289
US-08-418-782-20
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05/08/418,782		
IS FORTON: WITED IS	99 GOCOACCOGGOGGAGATTGTCAGGGTAATGGCAGTCCCTGCCGTTGCCGTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTATACCCCTACCATGGCCCGGCCGG	ATGCCTCTGCGTTAGCCCCTGACCCA 939 
i: 30.440 HRBER 150.141US1 OGRAFION:	99 940 AAAGCTCTGACGTGAAACCAGGGCTTAGGTGGGGCAACCCCAACATGCAGGGAAG  Db 934 GAGGTGCTCGGCTGGACCAGATGGGTTGGGTTGGAAACCTGGTATGGCACGGAAC	SGGGAACCCAACATGCAGGGGAAG 999 
061.51 102.20: 1155:	99 1000 GCAAGCAAGGGGGGGGGGTACGAAGGGGGTGGACCACCAACAAAATC Db 994 GGTAAGGAGGGAGCAGCAGCAGGAGGGTATGAAGAAAAAACACCCCAGAAAATI	TITGGACCACCACGAAATIC 1059 
110	09 1060 GATATGGGCTATTTCGACCTGGTGTTCGGGTACATTGGGAACTGAAAAAGGGTCGTGCC Db 1054 GACAACAGTTTCCGAAGATCTGTACGGTACGGAGTGGAGCGCTGACGAACACCTTGACCAACAGCCTTGACCAACAACACCTTACCAACAACACCTTACCAACAACACCTTACCAACAA	ATTGGGAACTGAAAAGAGTCCTGCC 1119                          AGTGGGAGCTGACGAAGAGCCCTGCT 1113
	OY 1120 GGTGCCCACCATTGGGAACCGATTGACATCAAAAAGGAAAACAAGCGGTTGACGCCAGC	AGGAAAACAGCCGTTGACGCCAGC 1179
27.3%; Score 618.6; DB 1; Length 2331; 58.7%; Pred. No. 4.6e-164; tve 0; Mismirches R19; Indela 63; Gans R.	OY 1180 GACCCTCTATTCSCCACAACCCGATCATGACCGATGGGGATAAGGCGATAAAGGTAAT	ATGCGGATATGGCGATAAAGGTAAAT 1239 
CGGAAGGGTTGAACCTGGATATTTTGCATCAGCAAGATCGCAAA 21	QY 1240 CCGACTIATGGGGCTATCTGGGAAAATTCATGGCGGATCCTGAGTACTTCAAGAAAACT  Db 1231 CGGATCTATGAGGGGAATACGGCTGGCTGGAACCCCCGAAGAAATTGGCCGAGGGA	CCGATCCTGAGTACTTCAAGAAACT 1299                    NACACCCCGAGGAATTGGCCGACGAG 1290
GANCGGATTTCAACTACGCTCAACTACGCTCCAATTCAACTACGATTCAACTACGATTCAACTACGATTCAACTACGATTCAACTACGATTCAACTACGATTCAACTACGATTCAACTACGATTCAACTACGATTCAACTACGATTCAACTACAACTACGATTCAACTAACT	0y 1300 TTCGCGAAGCGTGCTTCAAGCTGACGCGGACCTGGGCCCGGAAATCACGTTACATC  Db 1291 TTCGCCAAGCCTGGTACAAGCTGATCACCACGAAAAACAGGGTCCGTTACAAGTACCTT	ACTGGGCCGAAATCACGTTACATC 1359 
	OY 1360 GGCCCGGAAGTGCCGCAAAGACTGATTGGCAAAACCCGATTCCGGCAGTAACACC	AGARCCGGTTCCGGCAGGTAACACC 1419
	dy 1420 dactactegeaagagges	AGCAGAAAATTGCACAAAGTGGCCTG 1467 
CGTGGGGGGGGGGGGGGTAACCGGAAGCCAGCGCTTTGCACCGGTCAACCG 459    C	Oy 1468 AGCATTAGTGAGTGGTCCCACGCTTTGGACAGTGCCCGTACTTATCGCGGTTCCATT Db 1471 ACTGTCTCACAGTTTCGACCATGGGCGCGGGGGTCGTCGTTCGT	### ##################################
	QY         1528 A19CGCGGCGGTGCTAACGGTGCCCGCATTGGCTTGGCCCCAAGAACGAGGC 1587           1	GGCCCCACAGAACGACGCGCGCGCGCGCGCGCGCGCGCG
	0y 1588 AACSACCGAA CCGCCTGGGGAAAGTGCTGACGACGACGACATCT	SCCTCTACGAGGAGATCT 1636 
CCTGCTFACGCTTCTCTTTCGCCCGCGCTCAFTTTGGGAACCCGA 639 AAAACCTTTCTTTTCGCTTTCTGCTTTCGTTTCGCTTTCGTTTCGCTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTTT	Oy 1637	CCATCGCGGACGTGATCGTTCTGGCC 1680
TGGGGTGAGGAAAAGAGGGGGGTGGCACTTCTGAGGAACGTGCGC 699	0y 1681 GGTAGCGTAGGCATCGAGAAAGCGGGAAAAGAGGGGGTACGATGGTGGGGTTCCGTTC  Db 1711 GGCTGGCGCCATAGAGAAAAGAGAGGGGGGGGGGGGCGCCACAAAACACGGCCCCAAAAAA	AGGTTACGATGTGCGCTTCCTTC 1740
	OY 1741 CTGAAAGGCCGTGCGATGCGACGCCGAAATGACCGAGACTCCTTGGGACCGCTG	CCACGCAGACTCCTTCGCACCGCTG 1800 
	OY 1801 GAGCGCTGGCCGATGCCTTCCGCAACTGGCAGAAAAAGAGTATGTGGTGAAGCCGGAA 1860	GGAAGGGTATGTGGTGAAGCCGGAA 1860 
	Qy 1861 GAGNIGCTGGATCGTGGGCGCAGCTGATGGGCTTAACCGGCCCGGAAATGACCGTGCTG 1920	NACCGGCCCGGAAATGACCGTGCTG 1920 

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Matches 1953: Conservative O: Mismatches 819: Indels 63: Gans R.	160 AACAAAGATTGGTGGCCGGAAGGGTTGAACTGGATATTTTGCATCAGCAAGATCGCAAA 21	172 AACCAGGACTGGACGGCTCAATCTGAAGGTACTGCACAAAACCCGGCGTC 231	TCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCTCGATTTCGAC	232 GETGACCCGATGGGTGCGGCTGTTCGACTATGCCGGGGGGGG		TGGGGGCACTACGGCGGTTGGATCCGTATCGCTTGCACTCCGCTGGCACCTACCGT   11   11   11   11   11   11   11	352 TACGGCCACTACGGGCCGCTGTTTATCCGGATGGCGTGGCGCTGCCGGCACCTACCGC 411 400 ATTGCTGATGGCCGTGGGGGCGCTGGTACCGAAGCCAAGGCATTACACTCGTCAACTCC 459	HI	460 TGGCCGGACAACGTCAGCTGGATAAAGCGCGCCGTCTGCTGGCCCGATCAAGAAGA 519 47 THGCCCGAAAGCCAGCTGGAAAGAAGCAG 531	520 TACGGCAACAAATCAGGTGGGCAGACCTGATGATTGCTGGCTG		580 TCCATGGGCTTACCGGCTTCTTTCGGCGGCGTCATATTGGGAACCCGAA 639	592 TCGATGGGCTTCAAGACGTTCGGCTTCGGCTGGCTCGGTCGACGAGGCCCG 649	AAAGATATCTACTGGGGTGACGAAAAAAAGAGTGGCTGGC	-AIGAGGILIAITGGGGGAAGGCACCTGGCICGGCGAIGAGCGITACAGC	700 GACGTGAACAAGCCAGAGACCATGAAAACCCGCGGGGGGGTGCCAATGGGTGTGARGC 759		754 TACGTGAACCCGAAGGCCGAACGCCAACCCGGACCCCATGGCCGGGGGGGCGGTCGACTT 813	CTTGAAACCTTCGCCCGTATGGCGATGAACGAAAAAACCGCAGCCCTCACAGCTGGC	CGCGAGACGTTTCGGCGCATGGCCATGAACGACGTCGAAACAGCGGCGCTGATCGTCGGC	880 GGCCACACCGTCGGTAATTGTCACGGTAATGCCAATGCCTTGGGTTAGCCCTGACCCC 939		ANGOCTICANOS TORNOS CANONIS CONTROL TORNOS TORNOS TORNOS CONTROL CONTR	GCAAGCAACGCGGTGACCTCGGGTATCGAAGGTGCTTTGGACCAACAAATTC	GGTAAGGACGCGATCACCAGCGGCATCGAGGACGACGACGACGAAATGG			1120 GGTGCCCACCATTGGGAACCGATTGACATCAAAAGGAAAACGAAACGAGCTTGACGCCAGC 1179		1180 GACCCTCTATTCGCCACACCCGATCATGACGATGCGCGATATGGCGATAAAGGTAAAT 1239	1174 GGCGGGCCAGGGCGCTCCCCGACGATGCTGGCCACTGACTTCTCGCTGCGGGTGGAT 1230
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Oy 1921 CTGGGCGGTATGCGGCAACTATGGTGGCACCAAACAACGGCGTATTCACC 1980	1951 GTAGGTGGCCTGCGCGTCTCGGCGAAACTACAGCGCTTACCGCTGGGCGTGTTCCCC		2011 GAGGCCTCCGAGTCACTGACCAACGACTTCTTCGTGAACCTGGTCGACATGGGTATCACC	UY 2041 FUGANGET - CGGTNAGGTRACCTACHCCTACAAATCGCCAAGACCGGTCCGTTC 2097  1		2131 AAGTGGACCGGCAGCCGCGGACTTGGGGTCCAACTCGGAGTTGCGGGCGTTT	OY 2.159 USAGANGTRAGGCCCAGGAGGGGGGGGGGGGGGGGGGGGGGCGCC 2217	Oy 2218 TGGACCAAAGTGATGACGCGATTCGACGT 2252	Db 2251 TGGGACAAGGGATGAACCTCGACAGGTTGACT 2285	RESULT 8 US-08-852-219-20	; Sequence 20, Application US/0885219 ; Patent No. 595731	; SERGAL INCREMIUN: ; APPLICANT: Tranklin R. ; APPLICANT: Kline, Bruce C.	APPLICANT: Uhl, James R. TITLE OF INVENTION: Discussion Strains	TITLE OF INVENTION: of M. Tuberculosis NUMBER OF SEQUENCES: 22 CORRESPONDENT ADDRES:	CONTROL MUNICIPAL & Gebhardt, P.A. CREDER 110 No. 60076754 Poweth Change of the Ann	ourth Street,	COUNTRY: USA  COUNTRY: USA  COUNTRY: DEADLE ENDER	CONFOLER AGAINMENT FORM: CONDINGED FORM CONDINGED TEN DO COMPANIETE CONDINGED TO THE DO COMPANIETE CONDINGED TO THE DO COMPANIETE CONDINGED TO THE DO COMPANIETE CONTRACTOR TO THE TENT TO	CONTAINS STATE TO COMPAGAINE OPERATING STATEM: PC-105/85-TOS SOFTWARE: Patentin Release #1.0, Version #1.25	CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/08/852,219	FILING DATE: 07-May-1997 CLASSIGATION: APPROXEMY ARGMENT INFORMATION:	NAME: Sandberg, Victoria A. REGISTRATION NUMBER: 41.287	REFERENCE/DOCKET NUMBER: 230.00010130 ; TELECOMMUNICATION INFORMATION:	; TELEPHONE: 612-305-1226 ; TELEFAX: 612-305-1228	; INFORMATION FOR SEQ 1D NO: 20; ; SEQUENCE CHARACTERISTICS:	LENGTH: 2331 base pairs	SYANDENESS: SINGLE SYANDENESS: SINGLE TO THE POPER THAN TO THE THE TO TH	FOULTONIA THE DATE OF THE PARTICLE OF THE PART	NAME ARE: CUS   LOCATION: 70.2289   US-08-822-21400	Query Match 27.3%; Score 618.6; DB 2; Length 2331;	58.7%; Pred.

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2152847 TCGANGGCTTTCAGACGTTCGGCTTCGGCTCGGCTCGACCAGTGGGAGCCCG-- 2152790
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                                                                                                                   APPLICANT: WHITE, Oven R.
APPLICANT: PENSER, Claire M.
APPLICANT: PENSER, Claire M.
TITLE OF INVENTION. IONA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS.
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27.3%; Score 618.6; DB 3;
Best Local Similarity 58.7%; Pred. No. 1.8e-162;
Best Local Similarity 58.7%; Pred. No. 1.8e-162;
Best Roches 1253; Conservative 0; Mismatches 819;
                                                                                                                                                                                                                FILE REPERENCE: 24166-20007.00
CURRENT PELLORION WINNER: US/09/103,840A
UNDER OF SEQ ID NOS: 298-06-24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various
OTHER INFORMATION: represent a, t, c or
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                         Sequence 2, Application US/09103840A Patent No. 6294328
                                                                               GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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                                                                                                                                                                                                                                                                                                                   AGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCGTACTTATCGCGGTTCCGAT 1527
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		CTTGANACCTTCGCCCGTATGCGATGANCGACAAAAACCGCAGCCTCACACCTGGC	GGCCACACCGTCGGTAATTGTCACGGTAATGCCATTGCGTTTAGCCCCTGACCA TI IIIII IIIIII IIIIII IIIIII IIIII IIIII	940 AAAGCCTCTGAGGTTGAAAACCAGGGCTTAGGTTGGGGCAACCCCAACATGCAGGGCAAG 999	1000 GCHAGCHACGTGACCTGGGTATCGAAGGTGCTTGGACGACCAACCCCACGAAATTC 1059	1060 GATATGGGCTATTTCGACCTGCTGTCGGCTACAATTGGGAAAAGAGTGCTGCC 1119	1120 GGTGCCCACCATTGGGAACGGATTGACATCAAAAGGAAAACGAGAGGGGGTGGCGGCGGT 1179 2152335 GGGCGTGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1180 GACCCTCTATTGCCACAACCGGATGACGGATGGGGATAAGCGATAAGGATAAAGTAAAT 1239 1180 GACCGCTCTATTGCCACAACCGGATGACGGATGAGGGATAAAGGATAAAGTAAAT 1239 115285 GGCGGGCCAGGGCGCTCCCCGACGATGCTGCCACTGACCTCTCGCTGCGGGTGGAT 2152209	1240 CCGACCTATCGGGCTATCTGCGAAAAATTCATGGCGGATCCTGAGTACTTCAAGAAAACT 1299 2152208 CCGACCTATGAGCGGATCACGCGGCGGAACACCCGAAGGAATTGGCGGAGGA 2152149	1300 TYCGCGAAGGCGTGCTTCAAGCTGACGCACCGTGGGCCCGAAATCACGTTACATC 1359 2152148 TYCGCCAAGGCGGTAACGTGAACCTGATCACCGTTGCAATACCTTT	1360 GCCCGGAACTGCCGGCAGAAGACCTGATTTGGCAAGACCGGATTCCGGCAGGTAACACC 1419 115088 GGGCGGTGGTCCCAAACCAGACCGCTGCGATCCGCACCTCCGCAACCGCACCTCCGCAACCACACACA	1420 GACTACTGCGAAGAAGTGG	1468 AGCATTAGTGAGATGGTCCACCGCTTGGGACAGTGCCCGTACTTATGGGGGTTCCGAT 1527 2151968 ACTGTCACAGATGTAGTTGACCCAAAGGGGGGGGGGGGG	1528 ATGGGGGGGGGTAACGGTGCCGCATTCGCTTGGCCCAAGAACGAAC	1588 AACGAGCCGGAGCCCTGGCGAAAGTGCTGAGCGTCTACGAGCATCT	1637	1351/86 TICHACTCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1741 CTGAAAGGCCGTGGCGATGCGACGGCGAGATGACCGACACAACAAACA	1801 GAGCCCGAGGCGCGCTCCCCAACACGCGCGAAGAAGGTATGCGGGAAGAAGTAGGGAAGGGAAGGAA
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                   Indels 64;
                                                                                                                                                                                                                                                                Length 2235;
                            COMPUTER: IMP PC Compatible
OPERATING STSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAYN: US/OS/418/782
                                                                                                                                                                                                                                                              Score 606.6; DB 1;
Pred. No. 1.1e-160;
0; Mismatches 819;
                                                                                                                               150.141051
                                                                                                ATTORNEY, CARENT INFORMATION:
MAME: WOGGSBEE, WALTON D.
REGISTRATION WIMBER: 30,440
REFERENCE/COCKET WORBER: 150.1
TELECOMONINICATION INFORMATION:
TELECOMONINICATION: 612-339-331
                                                                                                                                                                                                                                                             26.8%;
                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2235 base pairs
                     Floppy disk
                                                                                                                                                                                                                                                                        Best Local Similarity 58.6 Matches 1252; Conservative
                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                        CLASSIFICATION: 435
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	934	GCAAGCAAGGCGTGAAATTC CGGGTAAGGGTGCTGAACCACCAAGCCCAAAATTC 1059 
	1060	GATATIGGGCTATTICGACCTGCTGTTCGGCTACAATTGGGAACTGAAAAAGAGTCCTGCC 1119
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	1360	GGCCCGGAAGTGCCGGCAGAAGACCTGATTTGGCAAGACCCGATTCCGGCAGGTAACACC 1419
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^	1651 (	GGCTGTGCCCCATAGAGAAAGCAGCAAAGCCGGCTGGCCACAACATCACGGTGCCCTTC 1710
	1741 (	CTGAAAGGCCGTGGCGATGCGACGCGACGACGCAGACTCCTTCGCACCGCTG 1800
•	1711	ACCCGGGCCGCACGGATGCGTCGCAGGACAAACCGACGTGGAATCCTTTGCCGTGCTG 1770
		GACCCCTGGCCGATGCCTTCCGCAACTGCCAGAAGAAGACTATGTGGTGAACCCGGAA 1860
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Matches 1552; Conservative 0; Mismatches 819; Indels 64; Gaps 9; Matches 1252; Conservative 0; Mismatches 819; Indels 64; Gaps 9; 10 Accadantsorrected and accadant and accadant and accadant and accadant and accadant and accadant accadant and accadant acca		340 TAGGGGGGAATAAGGGGTTGAATAACGAAAGAGGGGGGGG	400 ATTOCTGATGGCCGGGGGGGGGGGGGGGGGGGGGGGGGGG	460 TGGCCGGAAAACGTGCGGATAAACGCGCGCGTCGTGTGTGCGCGTGCAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	520 TAGGGAACAAAAATCAGGTGGGGAGACGTGATGATGTGGGGGGGG	580 TCCATGGGCTTACCTGCTTACGGCTTCTTCGGCGCGCGAATTTGGGAACCCGAA 639 510 TILIIIII	640 AAAGATATCTACTGGGGTGACGAAAAGGGGGGGGGGGCACTTCTGACGAACGGAACGC 699 11	700 GAGGTGAACAAGCGAGACACACAGGAGAGGGGGGGTGCCAAATGGGTCTGATC 759 643 GGTAAAGCGGGAGTC	760 TATGTGAACCCGGAAGGTGTTAACGGCCACCTGATCCGCTGAGAACCGCACAGAGT 819 694 TACGTGAACCGGAAGGGCGAACGGAACCGGAACCGAAGGGGCGGACGAATT 753	820 CTTGAAACCTTCGGCGTATGGGGATGAACGAAGAAAAAACGGGAGCCTCACAGCTGGC 879 754 CCCAAAACGTTCGGCGAATGGCCAATGAACAAGAGCGAAACGGCGTATCGTCGAAAAAAAA	880 GECCACACGTGGGTAATTGTCACGGTAATGGCAATGCCATGGCGATGGCTGGGGTTAGCCCCTGACCC 939	940 AAAGCCTCTGACGTTGAAAACCAGGCCTTAGGTTGGGGCAACCCCAACATGCAGGGCAAG 999 874 CAGCTTCTCGCTGGACAGATGGCCTTGGGCGGGAACAACAACAGAACC 933	1000 GCAAGGCGCGTGACCTGGGGTATCGAAGGTGCTTGGACCACCAACCCCAACTGCAATTC 1059 11	1060 GATATGGGCTATTTGGACCTGCTGTTGGGAACTGAAAAGAGTGCTGGC 1119 994 GACAACAGTTCCTGGAAATGTGTATAGAAGGAGGAGGCTGT 1053	1120 GGTGCCCACCATTGGGAACGATGACATCAAAAAGGAAAACAAGCGGGTTGACGCCAGC 1179 1054 GCCGTTGGCAATACACGGCAAGAGGGGCGGGTGCGGGACCACATCCCGGACCGTTC 1113	1180 GACCCCTCTATTCGCCACACCCGATCATGACCGATATGGCGATAATGGCGATAAAGGTAAAT 1239
Be Ma	6 6	S G	è 9	SP 63	čo da	yo da	Qy Dp	, q <sub>Q</sub>	oy G	δδ Op	oy q	Qy	Qy Dp	Qy	oy ob	δλ
1861 GAGATCTGCTGGATCGTCGCTGATGGCCTAACCGGCCGGAATGACCTGCTG 1920   11111111111111111111111111111111111	Db 1950 GAGGCCTCCGAGTCAACGAACGACTTCTTCGTGAACTTCTTCGACATCCACCATCACC 2009  Oy 2041 TGGAACCCGGTAGGTAGCAACGCTACGAAATCCGGGAACGCGCACACGCGTGCCGTG 2097  Db 2010 TGGGAGCCTTCCCACAAATACGGGACTACAACGGCAACGATGGCAATTGCAAGTGCAACTGCAACAACGTG 2069					, U/ H4		NUMBER OF SEQUENCES: CORRESPONDENCE ADDRE ADDRESSEE: SCHWEG STREET: 3500 IDS	CITY: MINKRAPOLIS STATE: MINKREGTA COUNTRY INVESTRA		SOFTWARE: Patentin Forth Patentin #1.25 CURRENT APPLICATION DATA: APPLICATION UNBERS: US/08/228,662	CLASSIPTICATION: 435 ATTORIET/AEDENT INFORMATION: NAME: MOESSIME HARREN D HEADTY OF THE TOTAL TO A TO A TO A TO A TO A TO A TO	REPERMICE/DOCKET NUMBER: 150.1230S01 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 1000PANION: TELECOMMUNICATION 1000PANION:	HYPORACTION FOR SEC ID NO: 1: SEQUENCE CHARCTERISTICS: LEMENT: 2.735 SEEP PAIRS TYPE: MINICIPAL ACAD AND ACAD ACAD ACAD ACAD ACAD ACAD	SEŽĒ.	Query Match 26.8%; Score 606.6; DB 1; Length 2235;

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1114 GGCGGGCC----AGGGCGCTCCCCGACGATGCTGGCCACTGACCTCTCGCTGCGGGTGGAT 1170
                         CCGACCTATCGCGCTATCTGCGAAAATTCATGGCCGATCCTGAGTACTTCAAGAAACT 1299
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                                                                            APPLICANT: Cockettll, Franklin R.
APPLICANT: Kilne Bruce C.
APPLICANT: Uhl James C.
TITLE OF TWENTION: Detection of Isoniazid Resistant Strains
TITLE OF TWENTION: Of W. Tuberculosis
NORHER OF SEQUENCES: 22
NORHESPONDENCE ADDRESS:
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                                                                                                                                                                                                                              ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 5922575th Fourth Street, Ste.
CITY: Minneapolis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 230.00010130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEFAX: 612-305-1228
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APPLICATION NUMBER: US/08/852,219
FILING DATE: 07-May-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                 ; Sequence 1, Application US/08852219
; Patent No. 5922575
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NAME: Sandberg, Victoria A.
REGISTRATION NUMBER: 41,287
                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-305-1228
INFORMATION FOR ESC ID NO: 1
SEQUENCE CHARATTERICS:
LENGTH: 2235 base pairs
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Matches 1252; Conservative
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STRANDEDNESS: single
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                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                USA
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US-08-852-219-1
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1531 AACGACCCGACACGGGATCTGCCACCCCGGAAGACCCTGGAAGACTCACGGAGTCA 1590     1531 AACGACCCCGACCGGGACACACGGCACACCTGGGAATCCAGGAGTCA 1590     1537 AACGACCCGGGGACACACGGGCACACACGCGGACACGGGATCCATGGCCTACGCTTCGCCT 1690     1539 TTCAACTCCGGGGGGCGCGGGGAAAGTCCTTCGCCGACCTTCGCTGTCTT 150     1531 TTCAACTCGGGGGGCGCGGGGAAAGTCGTTCGCACGCACG	1801 GAGCGGCTGGCCGATCCGCAACTGGCAGAAGAAGAAGAAGAAGAAGCGGGAAGAAGAAGAAGA	DB 1991 GARGAGGCCTGCTGGG-GGAACTACAGGGTTACGGGGGGGTTACGC 1949  Qy 1981 GAATGTGAAGGCCGTTTTAGCCAAGCGCTTACGGGGGAACGC 2040  1950 GAGGCTGCGAGTCACTGACAACGACTTTTTGGAACCTGCTCGACGGAACAGC 2009  2041 TGGAAGCCGGTGGTAGGTAGCTACCTGACAAACCGGCGAACGGGGGAACGC 2009  Qy 2041 TGGAAGCCGGTGGTAGGAACCACTACGAAATCGCGAACAACGGGAACGGG 2097  101 11 11 11 11 11 11 11 11 11 11 11 11	0y   2098   AAGTGGACCCCCGGGGTGGATTTGGTTCCAACTCGCTACTGCGCTTTAC 2157   1   1   1   1   1   1   1   1   1	HSSULT 14  US-08-44B-78-2    Sequence 2, Application US/08418782   Patent No. 5658733   GENERAL INFORMATION:   APPLICANT: Cockerill, Frankin R.   APPLICANT: Cockerill, Frankin R.   TILE OF INVENTION: Discretion of Isoniazid Resistant Strains   TILE OF INVENTION: Of M. Tuberculosis   NUMBER OF SURPERION: Of M. Tuberculosis	ADDRESSES: Schwegman, Lundberg & Woessner STREET: 3500 INS Center CITY: Minneapolis STATE: Min COUNTY: USA COUNTY: USA COUNTY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: INM FC Compatible COMPUTER: INM FC Compatible SOFTWARE: Petentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/418,782
GGGAGACCTGATGATTCTGGCTGCCACCGTGGCTTATGGGGGGGG	## ## ## ## ## ## ## ## ## ## ## ## ##	Db 814 GTCACATTCGGTAAGACCCATGGCGCCGGCGCGCGCGACCGAC		1240 CCGACCTATCCCCCTATCTGCGAAAATTCATGCCGATCCTGAGTACTTCAAGAAAAT	1420 GACTACTGCGAAGAGCGG

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1871 TGGATCGTGCGCAGCTGATGGCCTTAACCGCCCGGAATGACCGTGCTGCTGCGCGCGTA 1930
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                                                        998 AGGCAAGCAACGCCGTGACCTCGGCTATCGAAGGTGCTTGGACCACCAACCCCACGAAAT
                                                                                    CCGGTAAGGACGCGATCACCAGCGCCATCGAGGTCGTATGGACGAACACCCCGACGAAAT
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                                                                                                                                                                                                                                              Length 2221;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                Score 578.2; DB 1;
                                                                                                                                                                                                                                                                          0; Mismatches 838;
                                                                                                                                                                                                                                                            Pred. No. 1e-152
                                                        150.141US1
                        NAME: Woessner, Warren D.
REGISTRATION NUBER: 30, 40
REPERRUCE/MOKEN NUMBER: 150.1
RELECOMMUSCATION HORBARTION:
TELECRAK: 612-339-3041
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              25.6%;
57.8%;
              ATTORNEY/AGENT INFORMATION:
                                                                                                                                         LENGTH: 2221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                          Best Local Similarity 57.8 Matches 1229; Conservative
CLASSIFICATION: 435
                                                                                                                                                                                        linear
                                                                                                                                                                                                      MOLECULE TYPE: DNA
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US-08-418-782-2
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1058 TCGATATGGGCTATTTCGACCTGCTGTTCGACTACAATTGGGAACTGAAAAAGACTCCTG 1117
989 GGGAACAACAGTTCCTCGAAAATCCTGTACAACTGGGAACTGGAACAGAAAAGCCTG 1048
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       400 ATTGCTGATGGCCGTGGGGGCGCTGGTACCGGAAGCCAGCGCTTTGCACCGCTCAACTCC 459
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                                                                                                                             340 TGGGGGCACTACGGCGGTTTGATGATCCGTATGGCTTGGCACTCCGCTGGCACCTACCGT
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GCCAGTTGACCAACGACTTTTTTGTGAACCTGACCGATATGGGGAACAGCTGGAAGC---
                                                                                                                                                 2108 CCTCGCGGGTGGATCTGGTATTTGGTTCCAACTCGCTACTGCGCGCTCTTACGCAGAAGTGT
                                                                                                                                                                                                                                                               ACCCCCAGGACGATAACGGCGAGAAGTTCGTCAGAGACTTCGTCGCCGCCTGGACCAAAG
                                   CGGTAGGTAGCAACGCCTACGAAATCCGCGCAACGACCGGTGCCGTGAAGTGGACCG
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APPLICANT. KINE BRUCE C.
APPLICANT. GILL JAMES R.
TITLE OF INVENTION DETECTION OF ISONIAID RESISTANT STRAINS
TITLE OF INVENTION: OF M. TUBERCUIOSIS
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STREET: 3500 LIS CENTER
CITY: MINERACULE
STATE: MINESOTA
COUNTY: USA
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COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
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Pred. No. 1e-152;
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NAME: WOESSERE, MARREN D.
REGIGTRATION WINBER: 30,440
REFERENCE/POCKET NUMBER: 150,123USO1
TELECOMMUNICATION INFORMATION:
TELECHONE: 612-339-0331
TELEFAX: 612-339-0331
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FILING DATE: 18-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08228662
Patent No. 5688639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 57.8%;
Matches 1229; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

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1 MENHKHSGSSTYNTNTGGKC......VKDFVKAWAKVMDLDRFDLK 745 US-09-884-889-8 4002 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	streptom		-	O31066 caulobacter	O9wxb9 legionella	_	_	_				P17750 salmonella	P13029 escherichia		073955 halobacter1	008404 mycobacteri				P00431 saccharomyc	-	P48534 pisum sativ			P56899 rhizobium m	. Q9le15 arabidopsis	P03341 baboon endo	P27189 escherichia	P36905 t amylopull	es	Q937f6 lactobacill	Q59637 pseudomonas	P39845 bacillus su
CHINAMACC		D.	CATB_STRRE	CATB_STRCO	CATA_BACST	CATA_CAUCR	CATA_LEGPN	CATA_MYCBO	CATA_MYCTU	CATA_MYCIT	CAT2_NEUCR	CATA_MYCSM	CATA_SALTI	CATA_SALTY	CATA_ECOLI	CATA_HALMA	CATA_HALN1	CATL_MYCFO	CATA_YERPE	CATA_ARCFU	CATA_RHOCA	CCPR_YEAST	APX1_ARATH	APX1_PEA	APU_THETU	NARG_BACSU	UVRA_RHIME	PER4_ARATH	GAG_BAEVM	TRC4_ECOLI	APU_THESA	YGJK_ECOL1	XPKA_LACPE	ODP1_PSEAE	PPS1_BACSU
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### ALIGNMENTS

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		(EC 1.11.1.6) (Catalase-peroxidase)	Streptomyces reticuli, Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales	Streptomyces.			Muller D.,	<del>-</del>	obiology 145:549-559(1999).	SIMILARITY).	CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.	3	SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY, BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.		gnc B	, F	s its conte	ξ								Hydrogen peroxide		RON (HEME AXIAL LIGAND) E21860AFE4B4A40E CRC64	6; DB 1;	128;
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                  ENHDAIVTDAKSEGSGG-CPVAHDRALHPTQGGG--NRQWWPERLNLKILAKNPAVANPL
                                        DPDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDG
                                                                               RGGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGF
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HENDLINE-21996410, PubMed-1200053;
HENLLEY S.D. Chater K.F. Cecrdeno-Tarraga A.-M., Challis G.L.,
Thomson N.K., James K.D.; Harris D.E., Quall M.A., Kloser H.,
                                                                                                                          Streptomyces coelicolor.
Bacteria: Actinobacteria: Actinobacteridae; Actinomycetales;
                                                                                                 Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
CPEB OR SCO0560 OR SCF73.07C.
Strepfomycas coelicolor.
                                                                                                                                                Streptomycineae; Streptomycetaceae; Streptomyces. NCBL_taxID=1902;
                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                     740 AA
                                     PRT;
                                   STANDARD;
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TFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGK

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PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMS 301

PDPIAAARDIRETFRRMAMNDEETVALIAGGHTFGKTHGAGPADA-VGDDPEAAAMEQQG

GAGAGTIPDAHDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLT 421

LGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKD 361

GGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKOKYGRKISWADLMILTGNVALETMGFK

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Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Banda C.H., Klaser T., Larke L., Warphy L., Oliver K., O'Neal S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A., Wictzorrek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.
                                                                                                                                                                                                                                                                    *Complete genome sequence of the model actinomycete Streptomyces
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PROSTIE; PS00435; PEROXIDASE_1: 1.
PROSTIE; PS00435; PEROXIDASE_4: 1.
OXIGOTGULCASE; PECOXIDASE_4: 1.
OXIGOTGULCASE; PECOXIDASE; TICD; HEME; Hydrogen peroXide;
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109 109 BY SIMILARITY.
272 272 IRON (HEME AXIAL LIGAND).
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InterPro; IPR002016; Peroxidase.
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Best Local Similarity
Matches 509; Conserv
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us-09-884-889-8.rsp

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ACT_SITE
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                         481
                                     601
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                                                                                                                                                                                                                                   --APELIPDAHDPAKKHRPRMLTTDLSLRLDPIYGPISRRFYENPEBFADAFARAWFKLT 417
                                                                         WASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKA 541
                                                                                                                                                                                                                      FVNILLDLNTKWRASDESDKVFEGRDFRTGEVKWSGTRVDLIFGSNSELRALAEVYGCADS 721
                                                                                   597 IGKGNRLPAEFLILDRANLLTLSAPEMTVLVGGLRVLGAGHQQSQLGVFTRTPGSLTNDF
                                                                                                                       VSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNY
                       HRDMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVSTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-FARCE 8005 / IAM11001,
STRAIN-FARCE 8005 / IAM11001,
LADLINE-899559121, PUMBed-25700997,
LADLINE-899559121, PUMBed-26700997,
LADLINE-89959111 STRAIN-89950 and expression in Escherichia coll of the Backlius stearchiermophilus peroxidase gene (pera).

J. Bacteriol. 171:4871-4875(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- FUNCTION: BIFUNCTIONAL, FXHIBITING BOTH A CATALASE AND BROAD-SPECTRON PEROXIDASE ACTIVITIES.
-I- CATALTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-I- COPACTOR: Binds 2 protchame IX and 2 Iron lons per tetramer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-29116998; Publed-9920270;
MEALS T. Miyal K., Trakulnaleaamsai S., Yomo T., Shima Y.,
Miki S., Yamsmoto K., Drabe I.;
"Evolutionary molecular engineering by random elongation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacilius stearothermophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus
                                                                                                                                                                                                                                                                                                                                                                                      ourreB-1996 (Rel. 33, Last sequence update)
FSFB-2003 (Rel. 41, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                          735 AA.
                                                                                                                                                                                                                                                                                   EEKFVKDFVKAWAKVMDLDRFDL 744
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01-FEB-1996
28-FEB-2003
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or send an email to license#isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 KPDPIAAARDIRETFGRMAMNDEFTVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEM 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 735;
                                                                                                                                                                                                                                                                               Oxidoreductase; Peroxidase; Iron: Heme; Hydrogen peroxide.
ACT_SITE 97 97 BY SIMILARITY.
ACT_SITE 101 101 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                         264 . IRON (HEME AXIAL LIGAND). 82989 MW; 7131204A4BFABEF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         139;
                                                                                                                                                                                                                                                                                                                                                                                                67.8%; Score 2714.5; DB 1.68.7%; Pred. No. 1.7e-169;
                                                                                                                                                                                                                                                                                                                                                                                                                                    75; Mismatches
                                                                      PRGE, MAGO2024; BAA37114.1; -
PIR, JSG520; JSG520;
PRSP, PRO411; TB39
ILLEPTO. IPRO0705; Pac_Ctase/prase.
ILLEPTO. IPRO0705; Pecoxidase.
ILLEPTO. IPRO0105; PECOXIDASE.
PRIMES, PRO0416; PECOXIDASE.
PROSITE; PRO0416; PECOXIDASE.
PROSITE; PS00045; PEROXIDASE.
PROSITE; PS00045; PEROXIDASE.]
PROSITE; PS00045; PEROXIDASE.]
PROSITE; PS00045; PEROXIDASE.]
                                                         EMBL; M29876; AAA22655.1;
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 68.7%
hes 511; Conservative
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735 AA;
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Gaps 14;

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75 IAAVKKDLAALMIDSQDWWPADYGHYGPPFIRMAWHSAGTYRIGDGRGGGGGGGGGRAPL 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 NIAGKCP-----MGHGRGPANRDWWPQSLRLEGINQHAPRSNPMGEAFDYAEAFKSLD 70
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                                                                                                        15 NTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKKLD 74
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                                                      DB 1; Length 737;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                 RON (HEME AXIAL LIGAND).
D900742D04E02E97 CRC64;
                                          67.2%; Score 2691; DB 1;
                                                                                   145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                   Pred. No. 5.9e
64; Mismatches
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       BY SIMILARITY
               IRON
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     106 BY
268 IR
80165 MW;
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Bacteria, Proteobacteria, Ga
Legionellaceae, Legionella.
                                                                   al Similarity 69.5
508; Conservative
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   106
268
737 AA;
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16-OCT-2001
28-FEB-2003
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09WXB9;
   ACT_SITE
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SEQUENCE
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                                                                                                                                                                                                                                       STRAIN-AFCC 19089 / CB15;
STRAIN-AFCC 19089 / CB15;
Stealman H. W., Parced F., Welnstein L.;
Catalase-peroxidase of Caulobacter crescentus: function and role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- CATALYTIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.
-1- COFACTOR: Binds 2 protoheme IX and 2 iron ions per tetramer (By
                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- INDUCTION; By hydrogen peroxide.
--- SIMILARIY: BELONGY TO THE PEROXIDASE FAMILY. BACTERIAL.
FEROXIDASS/CATALASE SUBFAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stationary phase survival.";

J. Backeriol. 179:681-6886(1997).

-I. FUNCTION: BIFONCTIONAL, EMIBITING BOTH A CATALASE AND BROAD-SPECTION PERONANCES ACTIVITIES.

BROAD-SPECTION PERONANCES ACTIVITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
PERES-2003 (Rel. 41, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                        737 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
            ::||||:||: || |||: ||||| 725
702 NQEKEVRDFINAWKVMNADRFDL 725
SEEKFVKDFVKAWAKVMDLDRFDL 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002016; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE005967; AAK25005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF027168; AAC45850.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-494 FROM N.A.
                                                                                        STANDARD:
                                                                                                                                                                              Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A87626; A87626.
PIR; T45480; T45480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00431; 1RYC.
TIGR; CC3043; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
ACT_SITE 102
                                                                                                                                                                                                                    NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
                                                                                      CATA_CAUCR
031066;
721
                                                                          CATA_CAUCR
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366

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434

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                                                                                                                                                                                                                                                                                                                                                   HEYMEN, AZZATIP, M., HONOTE N., COLE S.T.;
MASSANDES MUTCHOIN IN the cachalase-proxidase gene, katG, are assistances mutchtoins in the cachalase-proxidase gene, katG, are assistance mutchtoin in the cachalase proxidase gene, katG, are many factobiol, 15:253-245(195).

MACHORION BERNONTONE, EXHERITING BOTH A CATALASE AND BRAD-SERVENE, EXHERITING BOTH A CATALASE AND INTRACELLIAR SURVINAL OF MYCOBACTERIA (BY SHALLARITY).

-1-CATALYTIC ACTULIAR SURVINAL OF MYCOBACTERIA (BY SHALLARITY).

-1-CORALYTIC MACHUMEN (PRODADIA).

SUBUNIT: Homodimen (Probable) IX and 2 Iron lons per tetramer.

-1 SIBILIARIT: BELONGY OF HIR PEROXIDASE FAMILK. BACTERIAL PROXIDASE FAMILK. BACTERIAL
                                                                                                                                                                                                                             453 ANDIANLKGKILNSGLTTSELVKTAWASASTFRGTDMRGGANGARIRLAPOKDWPANDPO
                                                                                                    DATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMR
                                                                                                                                                                                                                                                                                                                VLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSG
                                                                 517 QLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                          697 TRYDLIFGSNSELRALAEYYGCADSEEKFVKDFVKAWAKVMDLDRFDLK 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomyoetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000763; Bnc_ctase/prase.
InterPro; IPR000705; Bnc_ctase/prase.
InterPro; IPR0007016; Parcardiase.
PRIME; PR0041; peroxidase; 1
PR057TE; PR00436; PEROXIDASE.
PR057TE; PS00436; PEROXIDASE.
PR057TE; PS00436; PEROXIDASE.
INTERPORTE; PS00436; PEROXIDASE.
INTERPORTE; PS00437; PEROXIDASE.
INTERPORTED PROXIDASE.
INTERPORTED PROXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32 Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-TBB-2003 (Rel. 41, Last annotation update).
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8231F0FF35397908 CRC64;
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BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BCG;
MEDLINE-95264910; PubMed-7746145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seqt
28-FEB-2003 (Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  740 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATA_MYCBO
                                                                                                                                                                                      577
                                                                                                                                                                                                                                                                                                                637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENDIBGLEARTILESGLTVSELVSTAWASASTFRNSDERRGGANGARIRLAPQRDWEVNNPQ 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 YGHYGPPFIRMAWHSAGTYRIGDGRGGGGGGGGGRRAPLNSWPDNANLDKARLLLWPIKQK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 FENLFGYEWELTKSPAGAYQWKPKDGAGAGTIPDAHDPSKSHAPFWLTTDLALRMDPDYE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 LONLFNFNWVKTKSPGGAIQWVPENSNASSMVPDAFDPSKRHAPVMLTTDLALKFDPVYS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGNYGPLFIRMSWHAAGTYRIYDGRGGANGGFQRFAPQNSWPDNANLDKARRLLWPIKQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGRKISWADLMILTGNVALETMGFKTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 RELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDIRETFGRMAMNDEETVALIAGGHTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                (By
                                                                                                                                               "Legionella pneumophila catalase peroxidase gene.";
Submitted (SEP-1989) to the EMI-ZeenamivDDBD databases.
--- FOUNCTION: BIFOUNCTIONAL, EXHIBITING BOTH A CATALASE AND
BROAD-SPECTRUM FROXIDASE ACTIVITIES (BY SIMILARITY).
--- CATALATIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
--- COFACTOR: Binds 2 protoheme IX and 2 iron lons per tetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                    -:- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; Peroxidase; Tron; Heme; Hydrogen peroxide.
ACT_SITE 104 104 BY SIMILARITY.
ACT_SITE 108 108 BY SIMILARITY.
ACT_SITE 170 770 INON (HRME AXIAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
IRON (HEME AXIAL LIGAND).
19E7931C472973C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.1%; Score 2564; DB 1; 66.4%; Pred. No. 1.2e-159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PP00141; peroxidase; 1.
PRINTS, PR00485; PEROXIDASE.
TICREAMS, TIGRO0196; Cat.per.HFI; 1.
PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
                                                                                                                         Watanabe H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB017595; BAA78342.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82914 MW;
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                                                                                                                     Amemura-Maekawa J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4SSP; P00431; 1RYC
                                                                                                                                                                                                                                                                                                                                              similarity).
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Unayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weldman J., Rhourl H., Gill J., Mikula A.,
Bishai W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               å
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SEQUENCE FROM N.A.

STRININE-982587; PubMed-9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Davies R., Davien D., Eron D., Chillingworth T., Conner R., Badcock K., Rasham D., Brown D., Chillingworth T., Conner R., Horris R., Davies R., Fathell T., Gentles S., Hamin N., Holroyd S., Harris S., Seegar K., Kroch A., McLean J., Moule S., Murphy L., A. Allver S., Seegar K., Kroch A., McLeam M.A., Rogers J., A. Sulston J.S., Taylor K., Whitchead S., Barrell B.G.; B., Coulder S., Sulston J. S., Seegar R., Skelcon S., Saures R., Sulston J.S., Taylor K., Whitchead S., Barrell B.G.; E., Markels S., Saures R., Sulston J.S., Taylor K., Whitchead S., Barrell B.G.; E., Markels S., Saures R., Saures S., Saur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris
                                                        Hoym B., Zhang Y., Poulet S., Young D., Cole S.T.;
Chrartcterization of the katt gene encoding a catalase-peroxidase
"Controcterization of the Nation Succeptibility of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-TOC. 25618;
STRAIN-TOC. 25618;
COCKELII F.R., UNI J.R., Temesgen Z., Zhang Y., Stockman L.,
ROBERTS G.D., WILLIAME D.L., KILDB B.C.,
Rapid Identification of a point mutation of the Mycobacterium
tuberculosis catalose-peroxidase (kat6) gene associated with
isoniazid resistance.
Supmitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H., Huovinen P., Viljanen M.K.;
in isoniazid-resistant Mycobacterium
isolated from Finnish patients.";
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang Y., Heym B., Allen B., Young D., Cole S.T., The catalase peroxidase gene and isoniazid resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND ISONIAZID RESISTANCE
                             MEDLINE-93308108; PubMed-8320241;
Heym B., Zhang Y., Poulet S., Your
                                                                                                                                      tuberculosis.";
J. Bacteriol. 175:4255-4259(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-H37Rv;
MEDLINE-92365822; Pubmed-1501713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-INH resistant strains;
Marttila H.J., Soini H., Huov
"katG gene mutations in ison!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.";
Nature 358:591-593(1992).
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                                                                                                                                                                                                                                                                                                       Submitted (SEP-1994)
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Cole S.T.;
                                                                                                                                                                                                                        REVISIONS
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                                                                                                                                                            EQHPPITETTIGAASNG-CPVVGHMKYPVEGGG--NQDWWPNRLNLKVLHQNPAVADPMG
                                                                                                                                                                                                                        PDFDYAEEFKKLDLAAVKKDLAAIMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGR
                                                                                                                                                                                                                                                                                                                             GGGGSGSGRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFK
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OBB129: 008211: 020544: 020546; 050531; 050553; 050554; 050555: 057215: 057274: 050546; 050551; 050552; 057215: 057274: 050556: 057275: 057215: 057274: 050556: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 057275: 
                                                           10;
   Length 740;
                                                           Indels
   Score 2544; DB 1;
Pred. No. 2.3e-158;
                                                        88; Mismatches 168;
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64.3%;
                                                           Conservative
                          Similarity
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60 AAFDYAAEVATIDVDALTRDIEEVMTTSOPWWPADYGHYGPLFIRMAWHAAGTYRIHDGR 119
                              GGGGSGSQRFAPINSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFK 181
                                              TFGFAGGRADVWEPEEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGK 241
                                                                                                      TEGEGEGEVDQWEPDE-VYWGKEATWLGDERYSGKRDLENPLAAVQWGLIYVNPEGPNGN 238
                                                                                                                                           PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMS 301
                                                                                                                                                          LGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELIKSPAGAYQWKPKD 361
                                                                                                                                                                                                              GAGAGTIPDAH-DPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKL 420
                                                                                                                                                                                                                                                                      THRDMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVST 480
                                                                                                                                                                                                                                                                                                                            NYIKPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSN 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCA 719
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MOTIS S.L., Neat J., Rouse D.A.,
"The catalase-peroxidase of Mycobacterium intracellulare: nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence analysis and expression in Escherichia coll.",
J. Gen. Microbiol. 1189.2563-2370(1992).
-!- FUNCTIONI. BIFUNCTIONAL, EXHIBITING BOTH A CAVALASE AND
INTRACELLULAR SUNVINAL OF MICOBACTREIA.
-! CARALITICA CATIVITY: 2 H(2)(2) = 0(2) + 2 H(2)).
-!- CORRECTOR: BINGS 2 protocheme IX and 2 iron ions per tetramer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase) (MI85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wycobacterium intracellulare.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                    746 AA
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                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Susiar Institute of Bioinformatics and the BMEL outstation the Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and its in no way entitled and this statement is not removed. Usage by and its in no way entitled and this statement is not removed. Usage by and its innownersal entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licensedsib-sib.ch).
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 DELETIONS OR DEFECTS IN KATG GENE CAUSE ISONIAZID
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                           SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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B43C033B533CDD89 CRC64;
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W -> G (IN INH-RESISTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%; Score 2544; DB 1;
64.3%; Pred. No. 2.3e-158;
tive 88; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
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15726/89)
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Interpro; IPR000763; Bac_ctase/prase.
Interpro; IPR002016; peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS, TIGRO1198; CAL_BEL_HPI; 1.
PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
PROSITE; PS50873; PEROXIDASE_4; 1.
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                                                                                                                                                                                                                                                                                                                                                                           EMBL; 297193; CAB10056.1; -
EMBL; AE007051; AAK46231.1; -.
EMBL; AF002194; AAB63371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
                                                                                                                                                                                                        140553 AAA83157 11
040595 AAA83150 11
041305 AAA83172 11
041307 AAA83172 11
041308 AAA83174 11
041310 AAA83176 11
041310 AAA83176 11
041311 AAA83176 11
041311 AAA83176 11
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740 AA; 80604 MW;
                                                                                                                                                                               EMBL; X68081; CAA48213.1; -.
                                                                                                                                                                                                                                                                                                         U41311; AAA85176.1; -. U41311; AAA85177.1; -. U41312; AAA85178.1; -. U41313; AAA85179.1; -.
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             (INH) RESISTANCE.
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ACT_SITE 104
ACT_SITE 108
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PDFDYAEEFRKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGR 121

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This STRS-PROT entry is copyright. It is produced through a collaboration between the Saisa Institute of Bioinformatics and the Emgi outstation—the Buropean Bioinformatics Institutions as long as its content is in no way modified and this statement is not removed. Usage by the forecast entitles and this statement is not removed. Usage by the for commercial entities are quirts a license agreement (See http://www.isb-sib.ch/announce/or send an email to license agreement (See http://www.isb-sib.ch/announce/
         LDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKF 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKDLAALMIDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGGGGGGGHPLNSWP 138
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DED01DC6D10BA582 CRC64;
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Neurospora.
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-- CAPALITIC ACTIVITY: 2 H(2)(2) -- 0(2) + 2 H(2)().

-- COFACTOR: Protoheme IX and iron (By similarity).

-- SIMILARITY: BELONGS TO THE PEROXIDASE PAMILY. BACTERIAL PEROXIDASE/CAPALASE SUBRAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Peroxidase/catalase 2 (EC 1.11.1.6) (Catalase-peroxidase).
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PERM: PROMIS; PROMISE:
PROSITE; PROMISE; PROMISE.
PROSITE; PROMISE; PROMISE.; 1.
PROSITE; PROMISE; PROMISE.; 1.
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es 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetidae, Sordariales, Sordariacese,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  753 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.1%; Score 2485.5;
62.1%; Pred. No. 1.5e
ive 93; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-22029357; PubMed-12033445;
                                                                                                                                                                                                                                                        VKDFVKAWAKVMDLDRFDLK 745
                                                                                                                                                                                                                                                                                               VEDFVAAWVKVMNSDRFDLK 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differentiation.";
Biol. Chem. 383:569-575(2002),
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753 AA;
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                                                                                                                              This SWISS-PROW entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the Employees the between the brincomatics Institute of Bioinformatics and the Employees on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by an its content are entitles are the experiment (so the property of the pr
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                                  SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
ACT_SITE 110 110 BY SIMILARITY.
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15F35F7F5028F2B2 CRC64;
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BY SIMILARITY
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InterPro; IPR002016; Peroxidase.
Homotetramer (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam. PP00141; peroxidase: 1.
HTMTS; PR00489; PEROXIDASE.
TICHRAMS TICRRO108; cat_per_HP1; J
PROXITE: PS00413; PEROXIDASE_1: 1.
PROSITE: PS00436; PEROXIDASE_2: 1.
PROSITE: PS00436; PEROXIDASE_2: 1.
PROSITE: PS50873; PEROXIDASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81417 MW;
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This SMISS-RROT entry is copyright. It is produced through a collaboration between the Poiss Institute of Bioinformatics and the EMBL outstation—the Burson horizon and the EMBL outstation—the Emblacement of the Emblacement is not profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a ciparies a license agreement (see http://www.isb-sib.ch/announco/or send an email to licensee agreement (see http://www.isb-sib.ch/announco/
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                                              -!- MISCELLANEOUS: DELETIONS OR DEFECTS IN KAIG GENE CAUSE ISONIAZID
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CORCIOR: Binds 2 protokheme ix and 2 iron ions per tetramer SUBRNIT: Homodimer (Probable).
                                                                        -!- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.
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                                            VYWGAETEWLGDK-RY------EGD------RELENPLGAVQMGLIYV
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analysis of isoniazid-resistant transposon mutants of Mycobacterium
anagmatis.";
Englast C. "falenfill, to the EMBL/GenBank/DDBJ databases.
Shumtted (APR-1997) to the EMBL/GenBank/DDBJ databases.
I PROFICION SIFFONCTIONAL, EMIDITING BOTH A CHALASE AND RROD-SPECTRON PROXIJASE AND CHALASE. MAY PLAY A KOLE IN THE INTERCELULAR SIGNALIA, FOR PROCESCIPERA.
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Corynobacterineae; Mycobacteriaceae; Mycobacterium.
RCBI_ERAID=1772;
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105957; 005763;
116-CGT-2001 (Rel. 40, Greated)
116-CGT-2001 (Rel. 40, Last sequence update)
116-CGT-2001 (Rel. 41, Last annotation update)
Peroxidase/catalase 7 (EC 1.11.1.6) (Catalase-peroxidase 7).
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STRAIN-ATCC 700084 / mc(2)155;
MEDLINE-97023930; PubMed-8870251;
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entitles requires a license agreement (See http://www.lsb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                     19;
                                    MRBL; AED16846; AMOTO1811; ...

DR InterPro; IPR000763; Bac_ctase/prase.

DR InterPro; PR000761; Peroxidase.

PEAR. PEO0141; Peroxidase.

DR PRINTS; PR00458; PEROXIDASE.

TIGRAMS; TIGRA0199; Cat_per_HPI. 1.

PROSITE; PS00435; PEROXIDASE. 1.

R PROSITE; PS00435; PEROXIDASE. 2.

R PROSITE; PS00435; PEROXIDASE. 2.

R PROSITE; PS00435; PEROXIDASE. 2.

M Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; ACT_SITE.

102 102 102 ...
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Matches 468; Conservative 83; Mismatches 166; Indels
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651
                                                                                                                                                                                 SNDFFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYG 717
                                                                                                                                                                                                 FRNY I KPEHKVSAEEMLYDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQL
                                                                                                                                     DNKAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADG
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STRAIN-CTERN N.A.
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PLOKAT D., Waln J., Whomson N.R., Pickard D., Waln J.
Churcher C., Mosham S. K., Chillingvorter, Commerceron P.,
Baker D., Baroks R., Chillingvorter, Commerceron P.,
Baker D., Baroks R., Furden N., Razzar J.,
Radion N., Barzar J.
Strain N., Bamin N., Happer N., Haren T.T., Holroyd S., Jagels R.,
Count N., Karsen T.S., Leether S., Woule S., O'Gaore P., Parry C.,
Mickohed G., Barrell N.G., Simmonda M., Skelton J., Stewens K.,
Mickohed G., Barrell N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-FOX PROPERTY ATC. 700931; STRAIN-FOX ATC. 700931; PARAIN-FOX ATC. 700931; PUDMed-12644504; MEDLINE-22531367; PUDMed-12644504; BELLIN MAYNEW G.P., Rose D.J., BORG M., Liou S. R.R., PULMERT G. III, MayNew G.P., Rose D.J., Burland V. Rodoylanni V., Schwartz D.C., Blattner F.R.; and Comparative genomics of Salmonella enterios serovar Typhi strains and CT18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i. SIMILARITY: Contains 1 heme regulatory motif (HRM) repeat.
                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Lest sequence update)
16-SEP-2003 (Rel. 43, Last annotation update)
Peroxidase/catalase HPI (EC 1.11.1.6) (Catalase-peroxidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBUNIS: Homocetramer (By similarity).
-i- SIMILANITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PROXIDASE PROXIDASE/CANALASE SUBFAMILY.
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                                                                                                                                                                                                                                                                  112 EDDSKEKFVKDFVAAWTKVMDADRFDV 738
                                                                                                                                                                                                                                                  CADSEEKFVKDFVKAWAKVMDLDRFDL 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Hydroperoxidase I).
KATG OR STY3760 OR T3510.
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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71 KKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGSGSQR 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGGTLPD 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 YIGPEVPKEDLIWODPLP---QPLYOPTOEDIINLKAAIAASGLSISEMVSVAWASASTF 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 THNTLSTGRCPFHQGGHDRSAGAGTASRDWMPNQLRVDLLNQHSNRSNPLGEDFDYRKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 FAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFKTFGFAGGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 DVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARD
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                                                                                                                                                                                                                                                                                                                       11 TYNTNIGGKCPFIGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEF
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                                                                                                                                                                                                                                                      DB 1; Length 726;
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                                                                                                                                                           -> P (IN REF. 1).
-> H (IN REF. 1).
-> K (IN REF. 1).
7C4BA44439E9FFAB CRC64;
                                                                     REF. 1).
                                                                                                                                                                                                                                                                        9.4e-152;
                                                                                                                                                                                                                                                                             84; Mismatches
                                                                                                                                                                                                                                                    61.0%; Score 2442.5;
63.5%; Pred. No. 9.4e
                      HUPZAKE
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726 AA;
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468; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latrellle P., Courtney L., Porvollik S., Ali J., Dance M., Du P., Hou S., Layman D., Lecnard S., Mayen C., Scott K., Holmes A., Grewal N., Mulyaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.; Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loewen P.C., Stauffer G.V.;
*Nucleotide sequence of kato of Salmonella typhimurium LT2 and characterization of its product, hydroperoxidase I.*;
Mol. Gen. Genet. 224:147-151(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X53001; CA477187.1;

EMBL; X100991, AAL22946.1;

PHSSP red80891, AAL22946.1;

HSSP red8034.1 ARK.

StyGene; SG10190; katG.

StyGene; SG10190; katG.

InterPro; IPR00075; Bac_ctase/prase.

InterPro; IPR000715; Peroxidase.

PERM; PR0014; Peroxidase.

PERM; PR0014; PEROXIDASE.

PROSTE; PS00045; PEROXIDASE.

PROSTE; PS00045; PEROXIDASE.1:

PROSTE;
                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Peroxidase/Catalase HPI (EC 1.11.16) (Catalase-peroxidase)
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BY SIMILARITY.
IRON (HEME AXIAL LIGAND).
                                                                                                       726 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                       STRAIN-LT2;
MEDLINE-91117169; Pubmed-2277629;
                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Salmonella
                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
710 FVAAWVKVMNLDRFDL 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).
                                                                                                       STANDARD;
                                                                                                                                                                                                                                               Salmonella typhimurium.
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106
267
                                                                                                                                                                                                            (Hydroperoxidase I).
KATG OR STM4106.
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ACT_SITE 102
ACT_SITE 106
METAL 267
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     NCBI_TaxID-602;
                                                                                                       SALTY
                                                                     RESULT 12
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72 KLDLAAVKKDLAALMIDSQDWWPADYGHYGPFFIRNAWHSAGTYRIGDGRGGGSGSGRF 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 VWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 RATEGNMGMNDEETVALIAGGHTLGKTHGAGPTSN-VGPDPEAAPIEEQGLGWASTYGSG 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                             12 YNTNTGGKCPFTGGSLKOSAGGGTKNRDWWPNMLNLGILROHSSLSDPNDPDFDYAEEFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 VWEPDLDVNWGDEKAWLTHRHPEA--LAKAPLGATEMGLIYVNPEGPDHSGEPLSAAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTG
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SPER-2003 (Rel. 41, Last sequence update)
15-8EP-2003 (Rel. 42, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                                                               A -> G (IN REF. 1).
24D32EBED5DE9BD6 CRC64;
                                                                                        IRON (HEME AXIAL LIGAND)
                                                                                                                                                                                                                                                                                   60.6%; Score 2423.5; DB 1, 63.6%; Pred. No. 1.6e-150; iive 78; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       730 AA
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                Matches 467; Conservative
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     102
106
267
20
20
621
     102
106
267
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621
726 AA;
                                                                                                                                                                                                                                                                                                                          Local Similarity
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059651;
     ACT_SITE
ACT_SITE
METAL
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                                                                                                                   REPEAT
CONFLICT
SEQUENCE
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CATA_HALMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-88314556, PubMed-3045098;
MEDLINE-88314556, PubMed-3045098;
Triggs-Raine B.L., Doble B.W., Mulvey M.R., Sorby P.A., Loewen P.C.
Triggs-Raine B.E., Doble B.W., Mulvey M.R., Sorby P.A., Loewen P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLIND-3334/765; PubMed-8346018, WEDLIND-3334/765; PubMed-8346018, VD. Daniels D.L., Blattner F.R.; Funkett G. III. Burland V.D., Daniels D.L., Blattner F.R.; Funkett G. Tar. Burland F. Daniels G. Tar. Burlandes G. Tar. Burland
                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tetramer
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Aniyels of the Escherichia coll genome. IV. DNA sequence of region from M9.2 to 92 a minuses, "good region from M9.2 to 92 a minuses," "good region from M9.2 to 92 a minuses," "good region from M9.2 to 11.5406-5417(1933).

I PARATYTIC ACHITICATAL SEASON (1683 to 100 to 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 heme regulatory motif (HRM) repeat.
                                                                                                              01-0CT-1593 (RGI. 37, Last sequence update)
20-FBS-2003 (RGI. 41, Last amocation update)
Peroxidase/Catalase HPI (EC 1.11.1.6) (Catalase-peroxidase)
(Hydroperoxidase I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- INDUCTION: By hydrogen peroxide.
-i- PANT The N-terminus is blocked.
-i- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
     726 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS, TIGRO198; CAL_DET_HPI; 1. PROSITE; PS00435; PEROXIDASE_1; 1. PROSITE; PS00435; PEROXIDASE_2; 1. PROSITE; PS50873; PEROXIDASE_4; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-K12 / MG1655;
MEDLINE-94089392; Pubmed-8265357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 170:4415-4419(1988)
                                                                             01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00141; peroxidase; 1. PRINTS; PR00458; PEROXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 309-726 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M21516; AAA24040.1; -.
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HSSP; P00431; 1CYF.
SWISS-2DPAGE; P13029; COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-339 FROM N.A.
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC43048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MG1655;
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                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
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809

668

728

us-09-884-889-8.rsp

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294 GNSKGGEMITSGIEGPWTQSPTEWDMGYINNLLDYEWEPEKGPGGAWQWAPKSEELKNSV 353
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                                                                                                   369 PDAHDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPR
                                                                                                                                                                                         429 VRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVSTAWASASTF
                                                                                                                                                                                                                                                                                                                                                          549 VLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              669 NIKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVKD
                                                                                                                                                                                                                                                                                                                       489 RNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609 SABEMLYDRAQLLSLSAPEMTALVGGMRYLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and Halobacterium salinarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHALDALILY).
SHALLARITY: BECONGS TO THE PEROXIDASE FAMILY. BACTERIAL
PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     073955; OSHHP5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last amorption update)
Percoxidase/Ostolase (RC 1.11.1.6) (Catalase-peroxidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
Els TaxID-6(091, 2242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NRC-1; PLASMID-PNRC200;
MEDLINE-20504483; PubMed-11016950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 RDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTY 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 GTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGAGTI 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (By
                                                                                                                                                   SEQUENCE FROM N.A., PARTILL SEQUENCE, AND MASS SPECTROMETRY.
MEDINE-9122366, PubMed-9924976;
Cannac-Caffrey V., Hudry-Clergeon G., Petillot Y., Gagnon J.,
Saccal G., Fransettl B.,
The profest sequence of an archaeal catalase-peroxidase.*;
Plochints 80:1003-1011(1998).
1- FOUNCINO: BIENCTIONAL, EXHIBITING BOTH A CATALASE AND
BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
1- CATALYTIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)).
1- COPALIYIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- NASS SPECTROMETRY: MM-81292; MM_ERR-9; METHOD-MALDI.
-i- SIMILARITY: BELONGS TO THE PEROXIDASE PAMILY. BACTERIAL
PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50873; PEROXIDASE_4; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
Haloarcula marismortui (Halobacterium marismortui).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
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5C7FFFE6C37ADC4B CRC64;
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BY SIMILARITY.
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InterPro. IFROUNGS. BAC_ctass/prase.
InterPro. IFROUNGS. BAC_ctass/prase.
Fram: PROUGL4; PACOXIAGAS: .
PRINTS: PROUGL8; PEROXIALAS: .
PROSITE; PROUGL8; PEROXIALAS: .
PROSITE; PSOUGL3; PEROXIDAS: .
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91 91 BY
95 BY
258 258 IRC
730 AA; 81252 MW;
                                                                Halobacteriaceae; Haloarcula.
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                                                                                               NCBI_TaxID-2238;
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ACT_SITE
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Search completed: October 7, 2003, 19:43:04
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                                    between the Swiss Institute of Bioinformatics and the EMEL outstation—the European Bioinformatics institute of Pere are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial outlities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0458; PEROXIDASE.

TIGGRAMS, TIGGROUD91, cat_per_HPT; 1.

PROSITE; PSO0435; PEROXIDASE_1; 1.

PROSITE; PSO0437; PEROXIDASE_2; 1.

PROSITE; PSO0437; PEROXIDASE_2; 1.

PROSITE; PSO0437; PEROXIDASE_4; 1.

Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; Plasmid;
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BY SIMILARITY.
IRON (HEME AXIAL LIGAND).
FBB8823BCD3CB2F9 CRC64;
                                                                                                                                                                                                                                                          Interpro; IPR000763; Bac_ctase/prase.
Interpro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                  EMBL; AE005159; AAG20931.1; -. EMBL; AF069761; AAC23534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 AA; 80476 MW;
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HSSP; P00431; 1RYC.
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ACT_SITE 79
ACT_SITE 83
METAL 248 2
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60 NDPDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPPFIRMAWHSAGTYRIGD 119
                                                                                                                                                                   179
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                                                                                                                                                                                                                                                                                            211
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                                                                                                                                                                                                                                                                                                                                                                                                          IEEMSLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQ 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVSTAWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQ 536
                                             32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDNKAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAAD 596
                                                                                                                           8
                                                                                                        120 GRGGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMG
                                                                                                                                                                                       1 MENHKHS-GSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDP
                                          MENEDHNEGTS------DWWPNQLDLEILDQNSQQVDP
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ò 셤 ò a 597 GPRNYIKPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQ 656

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657 LSNDFFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVY
                                                                               717 GCADSEEKFVKDFVKAWAKVMDLDRFDLK 745
                                                                                               692 GSDADEELFVQDFVDTWSEVMKLDRFDLE 720
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

; Search time 16.5881 Seconds (without alignments) 2134.727 Million cell updates/sec 7, 2003, 19:31:42; October Run on:

US-09-884-889-6

1 MNNASADDLHSSLQQRCRAF.....RDFVAAWTKVMNADRFDVAS 753 4058 Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

## SUMMARIES

		Description	P14412 bacillus st	7 mycobacte	087864 streptomyce	031066 caulobacter	<u>σ</u>		P17750 salmonella	Q8z303 salmonella	Q04657 mycobacteri	008404 mycobacteri	Q08129 mycobacteri		Q8x182 neurospora	Q9wxb9 leqionella		073955 halobacteri	Q9x6b0 yersinia pe			Q05431 arabidopsis			Q87rg0 vibrio para		Q9thx6 lycopersico			Q9ss67 arabidopsis	064207 mycobacter1	P07941 kluyvera ci	9	~	048677 arabidopsis
	f	ar	CATA_BACST	CATA MYCSM	CATB_STRRE	CATA_CAUCR	CATB_STRCO	CATA_ECOLI	CATA_SALTY	CATA_SALTI	CATA_MYCIT	CATI_MYCFO	CATA_MYCTU	CATA_MYCBO	CAT2_NEUCR	CATA_LEGPN	CATA_HALMA	CATA_HALN1	CATA_YERPE	CATA_ARCFU	CATA_RHOCA	APX1_ARATH	CCPR_YEAST	APX1_PEA	SYL_VIBPA	PE12_ARATH	TL29_LYCES	LIGC_TRAVE	NCO3_HUMAN	PE28_ARATH	VG14_BPMD2	PAC_KLUCI	PUR2_METAC	SLAP_BACLI	PER6_ARATH
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*	Query	Match	61.3	54.6	53.4	53.3	53.0	51.6	51.4	51.3	50.9	50.5	50.3	50.2	49.4	49.3	49.2	47.6	47.4	46.9			6.1	•	3.0		5.0		2.8	2.8	2.7	2.7	2.7	2.7	2.7
		score	2489	2216.5	2168.5	2162.5	2149.5	2095	2086	2083	2063.5	2050	2042.5	2036.5	2003	2002	1998	1930	1922.5	1901.5	1642.5	267	248.5	245.5	121	118	117	113.5	113.5	112	111.5	111.5	9	108.5	108
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Interpro; IPR000763; Bac\_ctase/prase. Interpro; IPR002016; Peroxidase.

PIR; JS0520; JS0520. HSSP; P00431; 1BJ9.

EMBL; M29876; AAA22655.1; -, AB020234; BAA37114.1; InterPro; IPR002016; Peroxida
Pfam; PF00141; peroxidase; 1.

99K786 bacillus ha 70234 clostidium 77554 mycoplasma 106003 escherichia 001401 cryza astiv Pl6372 mis muscul 991499 naisseria 991499 crabidopsi 006575 escherichia 943872 erabidopsi 043872 erabidopsi 043872 erabidopsi
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SYL_BACHD GUNI_CLOTM DNJM_WCCPN CEAN_BOOLI GLB_ORYSA MUTA_WOUSE PEZ9_ARATH PRC_ECOLI PEG4_ARATH PEG4_ARATH PEG4_ARATH
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105 105 105 105 105 105 105 104 104 103 103 103 103 103 103 103 103 103 103
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ATCC 8005 / IAMI1001.
HEDLIRE-805-12: PUMMed-570897;
HEDLIRE-805-12: PUMMed-570897;
Licoling, nucleotide sequence, and expression in Escherichia coli of
the Bacillus stearchtermophilus peroxidase gene (PerA).*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trakulnaleamsai S., Aihara S., Miyai K., Suga Y., Yomo T., Negoro S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mat. Blotechnol. 17:58-61(1998).

**Nat. Blotechnol. 17:58-61(1998).

**Indication a Biffurcitonal, Extratring Borh a Catalase AND
BRONGTON BIFFURCITONAL, EXTRIBES.

**Indication CATIVITY: 2 H(2)(2) - 0(2) + 2 H(2)0.

**Indication CATIVITY: 2 H(2)(2) - 0(2) + 2 H(2)0.

**Indication CATIVITY: Brotechneme IX and 2 Lron ions per tetramer.

**Indication CATIVITY: BROOMS TO THE PREOXIDASE FAMILY: BACTERIAL

PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-99116998; PubMed-9920270;
Metsuura T., Miyal K., Trachinaleaamsal S., Yomo T., Shima Y.,
Mats., Yanamoto K., Urabe I.;
"Evolutionary molecular engineering by random elongation
"Indepensis";
                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus
                                                                                                                                                                          01-FPB-1996 (Rel. 33; Last sequence update)
28-FPB-2003 (Rel. 41, Last annotation update)
28-FPB-2003 (Rel. 41, Last Canton update).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Urabe I.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
                                                                        735 AA
                                                                        PRT;
                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
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28-FEB-2003
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                                                                   CATA_BACST
P14412;
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                                    CATA_BACST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 PRHRAIRER-----AMSGKCPVMHG--GNTSTGTSNKDWWPEGLNLDILHQQDRKS 74
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                                                                                                                                                                                                                                                                         STRAIN-FICC 700084 / mc(2)155;
BLDINE-97023930; PubMed-897021,
BILIman-3cobe H., Clopel R.L.;
"Analysis of isoniazid-resistant transposon mutants of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R PERMY PRODIAL; percenters.

R PINTS: PRODIAL; percenters.

R TIGREAMS: TIGRODIAS: Cac_per_HBI; 1.

BROSITE: PRODIAS: PERCENTONSE_1; 1.

BROSITE: PRODIAS: PERCENTONSE_2; 1.

BROSITE: PROSIAS: PERCENTONSE_4; 1.

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CONIGOTEGUCIASE; PERCENTONSE_4; 1.

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    16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2004 (Rel. 41, Last annotation update)
Peroxidase/catalase T (EC 1.11.1.6) (Catalase-peroxidase T).
                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98; Mismatches 198; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 PTRTA -> AHEDG (IN REF. 2).
81131 MW; A15A754A826FB5D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRON (HEME AXIAL LIGAND).
L -> M (IN REF. 2).
D -> RT (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.2e-147;
                                                                                                                                                                                                                     FEMS Microbiol. Lett. 144:47-52(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 Similarity 57.1
425; Conservative
                                                            Mycobacterium smegmatis.
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214 2
374 3
739 AA;
                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                      NCBI_TaxID=1772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTAQOVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQGLGWGN 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNMOGKASNAVTSGIEGAMTTNPTKFDMGYFDLLFGYNWELKKSPAGAHHWEDIDIKKEN 387
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                                                                                                                                                                                                               32 RERAMSGKCPVMHGGNT---STGTSNKDWWPBGLNLDILHQQDRKSDPMDPDFNYREEVR 88
                                                                                                                                                                                                                                           ONRONAAGCP-FHGSVTNQSSNRTTNKDWWPNQLNLSILHQHDRKTNPHDEEFNYAEEFQ 62
                                                                                                                                                                                                                                                                                                                                                    APLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVD
                                                                                                                                                                                                                                                                                                                                                                                                                  183 VHHPEEDVYWGSEKEWLA--SERYSGD----RELENPLAAVQMGLIYVNPEGPDGKPDPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGGSQRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 SYGKGKGSDTITSGIEGAWIPTPIQWDTSYFDMLFGYDWWLTKSPAGAWQWMAVDPDEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 KPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKSRYIGPEVPAEDLIWQDPIPAGNIDYCE---EVVKQKIAQSGLSISEMVSTAWDSART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          563 VGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWQRKEYVVKPEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1LDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWK
                                                                                                                                                                                       Gaps
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                                                                                                                                                                                       16;
                                                                                                                                                          Length 735;
    PRAIRIS FROMOSO PERMALANDE.
PROSITE: PROGRES: PERMALANDE.!
PROSITE: PROGRES: PERMAINSE_1: 1
PROSITE: PROGRES: PERMINASE_4: 1.
OXIOCOGGICARRES: PERMINASE_4: 1.
OXIOCOGGICARRES: PERMINASE_4: 1.
OXIOCOGGICARRES: PERMINASE_4: 1.
ACT_SITE 07 BY SHILLARITY.
ACT_SITE 07 BY SHILLARITY.
SACT_SITE 101 101 BY SHILLARITY.
SACT_SITE 104 101 BY SHILLARITY.
SACT_SITE 104 101 BY SHILLARITY.
SACT_SITE 104 104 BY SHILLARITY.
SACT_SITE 105 AN # 82999 MM; 71312044ABFABERI CRC64;
                                                                                                                                                      Score 2489; DB 1; Length 73:
Pred. No. 9.8e-167;
85; Mismatches 160; Indels
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PRINTS; PR00458; PEROXIDASE
                                                                                                                                                                       64.28:
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                                                                                                                                                                       Similarity
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135 ADGRGGGGTGSQRFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYES 194

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16-OCT-2001 (Rel. 40, Created)

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23;

us-09-884-889-6.rsp

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740 AA;
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                                                                                                                                                                                            AKAWFKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEEVVKQK--IAQSGLSIS 492
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                                                                                                                                                                                                                                                                                                                                                            FVNLTDMGNSWK---PVGSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVYAQDDN 728
                                                                                                                                                                                                                                                                                                                                                                      UNPEGVNGHPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPK
                                                                                         237 VNPEGPNGNPDPQASAIDIRETFGRMAMNDVETAALIVGGHTFGKTHGNGDASLVGPEPE
                                                                                                              ASDVENQGLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAG
                                                                                                                                                                 EMVSTAWDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPERLARVLSVYEQISADTG--
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                                                                                                                                                      AHHWEPIDIKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zou P., Borovok I., Ortiz de Orue Lucana D., Muller D., Schrempf H. The mycellum-associated Streptomyces reticuli catalase-peroxidase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTIÓN: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND BROAD-SPECTRUM PEROXIANAS ACTIVITIES (BY SIMILARITY).
-i- CARALTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-i- COPACTOR: Binds 2 protoheme IX and 2 Iron ions per tetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity.
-i-SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-027-2001 (Rel. 40, Created)
Cocr-2001 (Rel. 40, Last sequence update)
28-EB-2003 (Rel. 41, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase peroxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        740 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its gene and regulation by Furs.";
Microbiology 145:549-559(1999).
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MEDLINE-99231840; PubMed-10217488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces reticuli
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use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See bittp://www.isb-sib.ch/announce/or send an enail to license@isb.ch).
This SWISS-PROY entry is copylight. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBLO dustation the European Bioinformatics Institute of I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 VSPRHRAIRERAM -- - SGKCPVMHGG -- NTSTGTSNKDWWPEGLNLDILHQQDRKSDPMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDFNYREEVRKLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGTGSQRFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 AKAWFKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEE-----VVKQKIAQSGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 ISEMVSTAWDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVL----SVYEQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  547 ADTGA---SIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADGFRIWQKK EYVVK PEBMLLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERY - GDVNKPETMENPLAAVQMGLIYVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TFGFGGGRADVWEAEEDVYWGPETTWL - DDRRYTGD - - - RELENPLGAVQMGLIYVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGVNGHPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 VENQGLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 WEPIDIKKENKP---VDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Peroxidase: Iron; Heme; Hydrogen peroxide.
ACT_SITE 105 105 BY SIMILARITY.
ACT_SITE 109 109 BY SIMILARITY.
ACT_SITE 272 272 IRON (HBME AXIAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81345 MW; E21860AFE4B4A40E CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415; Conservative 114; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 2.9e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.4%; Score 2168.5; 55.3%; Pred. No. 2.9e
                                                                                                                                                                                                                                                                                                                                 EMBL; Y14317; CAA74698.1; -.
HSSP; P00431; TCA.
LILGEPTO; LPR000763; BAC.CTASG/PTASG.
LILGEPTO; LPR000701; PETOXIdASG.
PIGN: PP00141; PETOXIdASG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00198; Cat_per_HPI; 1. PROSITE; PS00435; PRROXIDASE_1; 1. PROSITE; PS00436; PROXIDASE_2; 1. PROSITE; PS50873; PEROXIDASE_4; 1.
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664 GOLTNDFFVNLTDMGNSWRPVGSN--AYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAE

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Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVAAWTKVMNADRFDVAS 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVIAWNKVMNADRLDLAA 737
                               102 B)
106 B)
268 II
80165 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                             102
106
106
737 AA;
                Complete proteome.
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Q9RJH9;
                                                                           SEQUENCE
                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                        153
                                                                                                                                                                                                                                                                                                                      132
                                                ACT_SITE
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licensetisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ANCO 1909 / CB15;
BIGGRID ANCO 1909 / CB15;
RIGHTANCO 1909 / CB15;
RIGHTAN W.C., Feblbyum.T.V. Laub.M.T., Detalesn I.T., Nelson K.E.,
Rightman W.C., Feblbyum.T.V. Laub.M.T., Obte N., Meddock J.R.,
Detocke I., Nelson W.C., Newton A., Stephens C., Phadden N.D., Ely B.
Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smil J., Craven M.B., Khouri H. Shetty J., Berry K.,
Rolonay J.T., Tran K., Wolf A., Vamathewon J., Ernelseva M., Milte o
"Stalberg S.L., Venter J.C., Shapiro I.L., Fraser C.M.;
Piroc. Netl. Nead. Sci. U.S.A. 98:4136-414(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steinman H.M., Fareed F., Weinstein L.; "Catalase-peroxidase of Caulobacter crescentus: function and role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stationary phase survival ",

J. Bacteriol. 179:6831-6836(1997).

-! FUNCTION: BINDERSTRING BOTH A CATALASE AND
BROAD-SECTION PROXIDASE ACTIVITIES.
BROAD-SECTION PROXIDASE ACTIVITIES.
-! CATALITIC ACTIVITY: 2 H(2)0(2) = 0(12) + 2 H(2)0.

-! COPACTOR: Binds 2 protoheme IX and 2 iron ions per tetramer (
                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;

    similarity).
    inOUCTION: By hydrogen peroxide.
    SINILARIT: BELONS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBPAMILY.

                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Percordasse/Cotalase (EC 1.11.1.6) (Catalase-peroxidase).
RATG OR CC3043.
                                                                       710 VYASDDAKEKFVKDFVAAWHKVMDADRFDL 739
                                                                                                                                                    737 AA
                                            722 VYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000763; Bac_ctase/prase
InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO199; CRL_PEL_HPI; 1.
PROSITE: PSO0435; PEROXIDASE_1: 1.
PROSITE: PSO0435; PEROXIDASE_2: 1.
PROSITE: PSSO0435; PEROXIDASE_4: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-494 FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-98012985; PubMed-9352936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE005967; AAK25005.1; -.
EMBL; AF027168; AAC45850.1; -.
PIR; A87626; A87626.
PIR; T45480; T45480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00141; peroxidase; 1. PRINTS; PR00458; PEROXIDASE.
                                                                                                                                                                                                                                                                                      Caulobacteraceae; Caulobacter
NCBI_TaxID=155892;
                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                         Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P00431; 1RYC.
                                                                                                                                                    CATA_CAUCR
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DALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGGGGRAPLN 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVDIWEP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 EKDIYMGDEKEWLAPSDERYGDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPLRTAQQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 VLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQGLGWGNPNMQG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 KASNAVTSGIEGAWTINPTKFDMGYFDLLFGYNWELKKSPAGAHHWE----PIDIKKENK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 KGPDAITGGPEVIWTQTPTRWSNHFFDNLFKYEWELTQSPAGAKQWQAKNAPADIP---- 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- DAFDPNKTHVPRMLTSDLALRFDPAYEKISRRFYENPDOFADAFARAWFKLTHRDMGP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAVVSDLHALMTDSQEWWPADFGHYGGLFIRLAWHAAGTYRITDGRGGAGGGQQRFAPLN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 PVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGP 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 KSRYICPEVPAEDLIWQDPIPAGNTDYCEE----VVKQKIAQSGLSISEMVSTAWDSART 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505 YRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQISADTGA-----SIADV 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 YRQSDKRGGANGARIRLAPQKDWAVNNPPVLAKVLAALEGVQKDFNASAGGGKKISLADL 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWQ--KKE 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540 IVLGGAAAIEKAAKDAGTSVTVPFAPGRMDASAEQTDAHSFEALEPRSDGFRNYRGPGKH 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           615 YVVKPEEMILLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNL 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDMGNSWKPVGSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVYAQDDNGEKFVR 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 ERAMSGKCPVMHGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDF 92
                                                                                                                                                                                                                                                                                                                               EDNIAGKCPMGHG----RGPANRDWWPQSLRLEGLNQHAPRSNPMGEAFDYAEAFKSLDL 71
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                               35;
                                                                                                                                                 DB 1; Length 737;
                                                                                                                                             Query Match 53.3%; Score 2162.5; DB 1; Length Best Local Similarity 56.3%; Pred: No. 7.5c-144; Matches 165; Conservative 103; Mismatches 185; Indels Matches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     j6-077-301) (Rel. 40. Created)
15-587-2001 (Rel. 40. Last sequence update)
15-587-2003 (Rel. 42. Last amnotation update)
Peroxidase/creatuse (EC. 11.1.1.6) (Catalase-peroxidase).
CPB3 OR SCOUS60 OR SCF73.07C.
                                                          IRON (HEME AXIAL LIGAND).
D900742D04E02E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               740 AA
BY SIMILARITY BY SIMILARITY
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866568
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435

491

530 604 590 664 650

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EGVNGHPDPLRTAQQVLETFARMANNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASD 317
                                                                                                                                                                                                                                                                                                                                      W----VAKDAPEIIPDAHDPAKKHRPRMLTTDLSLRLDPIYGPISRRFYENPEEFADAFA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 RAWFKLTHRDMGPKSLYLGPEVPEETLIWQDPLPEPEGEVIDAEDVATLKTKLLESGLSV 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLINDFFVNLIDMGNSWKPVGSN--AYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEV 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEMVSTAWDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYE----01SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548 DTGA---SIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 ECPNGNPDPIAAARDIRETERRMAMNDEETVALIAGGHTFGKTHGAGPADAVGDDPEAAA
                                                                                                                                           VENQGLGWGNPNMQGKASNAVTSGTEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHH
                                                                                                                                                                                                                                                                         WEPIDIKKENKPV -- DASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFA
                                                                                                                                                                                                                                                                                                                                                                                                       436 KAWFKLTHRDLGPRSRYIGPEVPAEDLIWQDPI--PAGNTDYCEEV--VKQKIAQSGLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGFRNWQKKEYVVKPEEMLLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
Analysis of the Escherichia coil genome. III. DNA sequence of the
region 1720 87. 2 to 89.2 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Baterobacteriaceae; Escherichia.
NCBL_PAXID-562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Analysis of the Escherichia coli genome. IV. DNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-007-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peroxidase/catalase HPI (EC 1.11.16) (Catalase-peroxidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94069392; Pubmed-8265357;
Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAQDDNGEKFVRDFVAAWTKVMNADRFDVA 752
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MEDLINE-89314956; PubMed-3045098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 21:3391-3398(1993).
                                                                                                                                                                                                                                                                                                               -
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MEDLINE-93347969; PubMed-8346018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-OCT-1993 (Rel. 27, Last sequ
28-FEB-2003 (Rel. 41, Last anno
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SEQUENCE OF 309-726 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydroperoxidase I).
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P13029;
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    258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Sulas Institute of Bioinformatics and the RMIS outstainnthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGTGSQRFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLP 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERY-GDVNKPETMENPLAAVQMGLIYVNP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEFDYARBAFBALDLAAVKRDIAEVLTTSQDWWPADFGNYGPLMIRMAWHSAGTYRISDGR
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                                                                                                                                                                                                                                             Benticy S. D., Chater K.F., Cerdeno-Tarraga A. H., Challis G.L.,
Thomson N. R., James K.D., Harris D. E., Quall M.A., Kleser H.,
Harper D., Batchan A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Batchan A., Brown S., Chandra G., Chen C.W., Collins M.,
Bunda C. H., Reser T., Larke L., Murphy L., Oliver K., O'Nell S.,
Benger K., Saunders D., Sharp S., Squares S., Taylor K.,
Benger N., Saunders D., Sharp S., Squares S., Taylor K.,
Bipmood D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND BROAD-SPECTRUM PERCYLDASE ACTIVITIES (W.S. STAILARITY).
-1- CATALIZE (ACTIVITY: 2 H(2)(2) - 0(2) + 2 H(2)A.
-1- COPACTOR: Binds 2 protoheme IX and 2 iron ions per tetramer (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Complete genome sequence of the model actinomycete Streptomyces colisolor A(2) = (1.4) \cdot (2002). Neture 4(1.1.4) \cdot (4.7) \cdot (2002).
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                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

    -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
PEROXIDASE/CATALASE SUBFAMILY.

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PROSITE; PSO0435; PEROXIDASE_2; 1.
PROSITE; PSO0437; PEROXIDASE_4; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 55.5%; Pred. No. 6.2e-143;
Matches 416; Conservative 111; Mismatches 192; Indels
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767C0A9BC9BD7798 CRC64;
                                                            Streptomycineae; Streptomycetaceae; Streptomyces.
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BY SIMILARITY
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InterPro: IRR002016; Peroxidase.
Pfan: PF00141; peroxidase; 1.
PRINTS: RF00458; PREMAIDASE.
TIGREAMS: TIGR00196; cat_per_HII; 1.
                                                                                                                                                                                                   STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed-12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL939106; CAB57412.1; -.
HSSP; P00431; 1A2F.
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coelicolor
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ACT_SITE 105 1
ACT_SITE 109 1
METAL 272 2
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                                                                                                                                                                   SEQUENCE FROM N.A
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713 687

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360 LLFGYNWELKKSPAGAHHWEPIDIKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAI 419
                                                                                                                                                                                               390 SRRFLNDPQAFNEAFARAWFKLTHRDMGPKSRYIGPEVPKEDLIWQDPLPQPIYNPTEQD
                                                                                                                                                                                                                                                                                  480 V---KOKIAQSGLSISEMVSTANDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPERLA
                                                                                                                                                                                                                                                                                                                                                                                                                                       568 MFELLEPIADGFRNYRARLDVSTTESLLIDKAQQLTLTAPEMTALVGGMRVLGANFDGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 NLFKYEWVQTRSPAGAIQFEAVD-APELIP-DPFDPSKRRKPTMLVTDLTLRFDPEFEKI
                                                                                                                                                             420 CEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEEV
                                                                                                                                                                                                                                                                                                                   KVLSVYEQISADTG-ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGVFTDCEGOLTNDFFVNLTDMGNSWRPV - GSNAYEIRDRKTGAVKWTASRVDLVFGSN
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MCGLINE-Z1534946; DibMcd.1507609;
MCGLINE-Z1534946; DibMcd.1507609;
MCGLINE-W. Sanderson K.E., Spieth J., Clifton S.W., Latrellle P.,
Courtney L., Porvollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Muyyon C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i-FUNCTION: Bifunctional, exhibiting both a catalase and broad-spectrum peroxidase activities.

-i-CAMALTIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.

-i-CORACTOR: Binds 2 protoheme IX and 2 iron ions per tetramer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-51117169, pubmed-2277629;
Locken P.C., Studifer G.V.;
Lockeolide sequence of Natio of Salmonella typhhmurium LT2 and
Characterization of 11s product, hydroperoxidase I.*;
Col. Gen. Genet. 24:147-151(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: Contains 1 heme regulatory motif (HRM) repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AuG-1390 (Rel. 15, Created)
28-FBE-2003 (Rel. 41, Last sequence update)
18-SEP-2003 (Rel. 42, Last annotation update)
Peroxidase/catalase HPI (EC 1.11.1.6) (Catalase-peroxidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     714 SLLRSYAEVYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   726 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-602;
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P17750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                508
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Best Local Similarity 53.4%; Fred. No. 4e-139;
Matches 405; Conservative 103; Mismatches 206; Indels 44;
                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 heme regulatory motif (HRM) repeat.
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THTRS: PRO0145; PEROXIDASE: 1
TICRRAMA: TICRRO198 cat_por_HPI; 1.
PROSITE: PS00445; PEROXIDASE_1; 1.
PROSITE: PS00445; PEROXIDASE_2; 1.
PROSITE: PS0045; PEROXIDASE_2; 1.
PROSITE: PS0046; PEROXIDASE_2; 1.
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24D32EBED5DE9BD6 CRC64;
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InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
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HSSP; P00431; LCYF.
SWISS-2DPAGE; P13029; COLI.
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106
267
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ACT_SITE 102
ACT_SITE 106
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-!- SIMILARITY: Contains 1 heme regulatory motif (HRM) repeat.
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--- SIMILARIY: BELOMS TO THE PEROXIDASE FAMILY. BACTERIAL
SERVIDASE/CRANAES SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhi
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This SWISS-PROW entry is copyright. It is produced through a collaboration between the fairst institution of Bioinformatics and the EMBI outstation the European Bioinformatics Institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseafsb-sib.ch).
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                                                                                                                                                                   Pfam: PF00111; peroxidase: 1.
PRETRYS. PROQUES; PEROXIDASE: 1.
PRESTRE, PS0045; PEROXIDASE. 1.
PROSITE, PS0045; PEROXIDASE. 1.
PROSITE; PS0045; PEROXIDASE. 1.
PROSITE; PS0045; PEROXIDASE. 1.
PROSITE; PS0045; PEROXIDASE. 1.
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                                                                                                  EMBL; AE008891; AAL22946.1; -.
PTR; S12039; CSEBHT.
HSSP; A48534; JARX.
STYGORE; SG10190; KatG.
InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
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                                                                                          EMBL; X53001; CAA37187.1; -.
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634
726 AA;
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                                                                                                                                                                                                                                      537 KVLSVYEQISADTG-ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDAD
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                                                                                                    V---KQKIAQSGLSISEMVSTAWDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPERLA
                                                                                                                                      HGVFTDCEGQLTNDFFVNLTDMGNSWRPV--GSNAYEIRDRKTGAVKWTASRVDLVFGSN
                                                                                                                                                                                                                                                                                                                                                                            SFAPLEPLADGFRNWOKKEYVVKPEEMLLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                          568 MFSLLEPIADGFRNYRARLDVSTTESLLIDKAQQLTLTAPEMTVLVGGMRVIGTNFDGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Waln a Churcher C., Murgall K.L., Bentley S.D., Holden M.T.G., Sebahia M., Baker S., Bentley S.D., Holden M.T.G., Sebahia M., Baker S., Bankan D., Brooks K., Chillingworth T., Connerton P., Connerton P., Connerton P., Connerton P., Dougles R.M., Dowd L., White N., Farrar J. T., Feltwell T., Hamila N., Haque A., Hien T.T., Holroyd S., Jagels K., Guall M., Larsen T.S., Leather S., Woule S., O'Gaora P., Parry C., Quall M., Rutherford K., Simmonds M., Skelton J., Stevens K., Complete genome sequence of a multiple drug resistant Salmonella entering aszoyat Typhi CT8**.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binds 2 protoheme IX and 2 iron ions per tetramer (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Peroxidase/catalase HDI (EC 1.11.16) (Catalase-peroxidase)
J. Bacteriol. 185:2330-2337(2003).
--- FWORTION: Biturictional, exhibiting both a catalase and broad-spectrum peroxidase activities (By similarity).
--- CATALYTIC ACTIVITY: 2 H(2)0(2) -- 0(2) + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               714 SLLRSYAEVYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             726 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21534947; PubMed-11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-SEP-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KATG OR STY3760 OR T3510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Hydroperoxidase I).
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420 CEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPEVPAEDLIWODPIPAGNTDYCEEV 479

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                   NGVPTDRPGVLSTDFFANLLDMRYEWKPTDDANELFEGRBRLTGEVKYTATRADLVFGSN 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 SNKDWWPEGLNLDILHQQDRKSDPWDPDFNYREEVRKLDFDALKKDVHALMTDSQEWWPA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWGHYGGLMIRMAWHSAGTYRIADGRGGGTGSQRFAPLNSWPDNVSLDKARRLLWPIKK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INRDWWPDQVDVSSLHPHSPLSNPLGDDFDYAAEFAKLDVEALKADMISLMTTSQDWWPA 99
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE PROM N.A.
MOLLINE-9212398; Pubmed-1336034;
MOTILS E., NALT J., Rouse D.A.;
"The catalage peroxidase of Mycobacterium intracellulare; nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence analysis and expression in Escherichia coll...,
J. Gen. Microbiol. 138 1364-370 (1992).
J. Gen. Microbiol. 138 1364-370 (1992).
J. Fen. Microbiol. 138 1364-370 (1992).
J. FENCTION SEPECTRON FRONTAINES FOUT VITIES. MY PLAY A ROLE IN THE INTRACELLULAR SURVIVAL OF MYCOBACTERIA.

J. CAPALYTIC ACTIVITY: 2 H(2)(2) - 0(2) + 2 H(2)0.
J. CAPALYTIC ACTIVITY: 2 H(2)(2) - 0(2) + 2 H(2)0.
J. CORACTOR: Binds 2 protocheme 1% and 2 iron ions per tetramer.
J. SUBUNIT: Homoretramer (Probable).
PEROXIDAR SURVIVALANES SUBFAMILY.
                                                                                                                                                                                                               01-0CT-1993 (Rel. 27, Created)
20-7CT-1993 (Rel. 27, Last Supulence update)
20-7CT-1993 (Rel. 21, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase) (MIB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 746;
                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterinae, Mycobacteriaceae; Mycobacterium.
NCBI_TAXID-1767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PROMASS PEROXIDARE_1] 1.
PROSITE: PROMASS PEROXIDARE_2] 1.
OXIGOTEURES: PROMASSE_2 1.
OXIGOTEURES: PROXIDARE; 1.
OXIGOTEURES: PROXIDARE; 1.
ACT_SITE 110 114 114 BY SINILARITY
ACT_SITE 1.
277 271 IRON (HENE AXIAL LIGAND)
SEQUENCE 746 AA, 81417 MH; 15F35F7F5028F2E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 6.7e-137;
98; Mismatches 197; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
TIGRFAMS; TIGR00198; cat_per_HPI; 1.
       = = ::
                                                                                                                                                                                                                                                                                                                       Mycobacterium intracellulare.
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395; Conserv
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CATA_MYCIT
ID CATA_MYCIT
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MI85.
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Matches 39
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between the Swiss Institute of BioInformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to itemseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 M-ENPLAAVOMGLIYVNPEGVNGHPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 CHGNGNASALAPDPKASDVENQGLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYFD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLFGYNWELKKSPAGAHHWEPIDIKKENKPYDASDPSIRHNPIMTDADMAIKVNPTYRAI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 NLFKYEWVQTRSPAGAIQFEAVD--APDIIPDPFDPSKKRKPTMLVTDLTLRFDPEFEKI 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 CEKFMADPEYFKKTFAKAWFKLTHROLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEEV 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 SRRFLNDPQAFNEAFARAWFKLTHRDMGPKARYIGPEVPKEDLIWQDPLPQPLYQPTQED 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 MIRMAWHSAGTYRIADGRGGGGGGGGRFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNRPET
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 726;
                                                                                                                                                                                                                                                                                Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                      B701C95343EEBB38 CRC64;
                                                                                                                                                                                                                                                                                                                                                    IRON (HEME AXIAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 406; Conservative 102; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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BY SIMILARITY.
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                                                                                                                   EMBL, AL627279; CAD09515.1; -.
EMBL, AE016846; AA071018.1; -.
EMTGFPC; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                         PFERM, PF00141; peroxidase; 1.
PRIATS; PR00458; PEROXIDASE.
TICHPAMS; TICH00198; CAL_DEL_HDI; 1.
PROSITE; PS00435; PEROXIDASE_11.
PROSITE; PS00436; PEROXIDASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
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79597 MW;
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726 AA;
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ACT_SITE 102
ACT_SITE 106
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           232
                                                                                                                                GGHSFGKTHGAGDADLVGPEPEAAPIEQQGLGWKSSYGTGSGKDAITSGLEVVWTPTPTK 334
                                                                                                                                                       FDMGYFDLLFGYNWELKKSPAGAHHWEPIDIKKENKPVDASDP--SIRHNPIMTDADMAI 410
                       GDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPLRTAQQVLETFARMAMNDEKTAALTA
                                                                               SGERE -- - LAQPYGATTMGLIYVNPEGPEGKPDPIAAAIDIRETFGRMAMNDEETAALIV
                                                                                                      GGHTVGNCHGNGNASALAPDPKASDVENQGLGWGNPNMQGKASNAVTSGIEGAWTTNPTK
                                                                                                                                                                                                       KVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPEVPAEDLIWODPIPA
                                                                                                                                                                                                                                                                             VDHELVDDNDVAALKKKVLDSGLSIPQLVKTAWSAAASYRNTDKRGGANGCRLRLQPQRS
                                                                                                                                                                                                                                                                                                     WQGNEPERLAKVLSVYEQISADTGA-----SIADVIVLAGSVGIEKAARAAGYDVRV
                                                                                                                                                                                                                                                                                                                             WEVNEPSELDKVLPVLEKIQQDFNASASGGKKISLADLIVLAGSAAVEKAAKDAGYEISV
                                                                                                                                                                                                                                                                                                                                                    PFLKGRGDATAEMTDADSFAPLEPLADGFRNWQKKEYVVKPEEMLLDRAQLMGLTGPEMT
                                                                                                                                                                                                                                                                                                                                                                  VLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWK - - PVGSNAYEIRDRKT
                                                                                                                                                                                                                                                                                                                                                                                                                         VLVGGLRALGANHGSSKHGVFTDRPGALTNDFFVNLLDMGTEWRASETAENVYEGRDRAS
           KYGNK ISWADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAVKWTASRVDLVFGSNSLLRSYAEVYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: BITUMCTIONL, EMHIBITING BOTH A CAPALASE AND BROAD-SPECTHUM PERSYLINGS FOUNDATIONS AND THE NOLE IN THE INTELLIGIAR SURVIVAL OF MICOBACTERIA (BY SIMILARITY).
CORALITOR CATILITY: 2 H(2)O(2) - (2) + 2 H(2)0.
CORACTOR: BIAGS 2 PICCORDER X and 2 Lion lons per letramer.
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Watti and kattir encode two different catalases-peroxidases
Wycobacestium fortuitum: ",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-027-2001 (Rel. 40, Created)
18-027-2001 (Rel. 40, Last sequence update)
18-027-2003 (Rel. 41, Last annotation update)
Peroxidase/catalase 1 (EC 1.11.1.6) (Catalase-peroxidase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homodimer (Probable)
SIMILARIY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
PEROXIDASE/CAPTALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 179:6880-6886(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 6841;
MEDLINE-98037481; PubMed-9371430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium fortuitum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAT1_MYCFO
008404;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWGHYGGLMIRMAWHSAGTYRIADGRGGGTGSQRFAPLNSWPDNVSLDKARRLLWPIKK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKFDMGYFDLLFGYNWELKKSPAGAHHWEPIDIKKENKPVDASDPSIRHNPIMTDADMAI 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 KVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 639 VLLGGMRVLGTNYGGTKHGVFTDCEGQLINDFFVNLTDMGNSWRP--VGSNAYEIRDRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLVGGLRALNTNHGGSKHGVFTANPGALSNDFFVNLLDMSTEWKPSETAENVYEGRDRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTNDSTNRELANPYGATTMGLIYVNPEGPEGKPDPLAAAHDIRETEGRMAMNDEETAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKWSNSYLEILYGYEWELTKSPGDAWQFEAKDAEAIIPDPFGGPP---RKPTMLVTDISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 GNTDYCEE----VVKOKIAQSGLSISEMVSTAWDSARTYRGSDMRGGANGARIRLAPQNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 VDHPLVDEQDIAALKEKLLDSGLSVQQLVKTAWSAAASFRGTDKRGGANGGRLRLQPQRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      579 PFLKGRGDATAEMTDADSFAPLEPLADGFRNWQKKEYVVKPEEMLLDRAQLMGLTGPEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDVNKPETME -- NPLAAVOMGLIYVNPEGVNGHPDPLRTAQQVLETFARMAMNDEKTAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGGHTVGNCHGNGNASALAPDPKASDVENQGLGWGNPNWQGKASNAVTSGIEGAWTTNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAVKWTASRVDLVFGSNSLLRSYAEVYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                             Heme; Hydrogen peroxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                  IRON (HEME AXIAL LIGAND).
B66BAD53DD26E70D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.5%; Score 2050; DB 1; 54.3%; Pred. No. 5.9e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 102; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                     Interpro; IPR000763; Bac_ctase/prase.
Interpro; IPR002016; Peroxidase.
                                                                                                                                                                                                                          PFGM, PF00141; peroxidase; 1.
PRIMIS: RR00485; PEROXIDASE.
TIGREAMS; TIGR00198; cac_per_HBI; 1.
PROSTIE; PS00435; PRROXIDASE_2; 1.
PROSTIE; PS00436; PRROXIDASE_2; 1.
PROSTIE; PS00873; PRROXIDASE_2; 1.
                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; Peroxidase; Iron;
ACT_SITE 113 113 BY SI
ACT_SITE 117 117 BY SI
                                                                                                                                                                                                                                                                                                                                                                                                                    83100 MW;
                                                                                                                                                   EMBL; Y07865; CAA69192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                  285 752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                        P00431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 388;
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ACT_SITE
METAL
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697 GQTRWTATANDLVFGSNSVLRAVAEVYAQEDNKAKMIEDFVAAWVKVMNNDRFDL 751
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S -> T (IN INH-RESISTANT STRAINS
H0181/94, H0452/92, H0948/92 AND
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W -> G (IN INH-RESISTANT STRAIN
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H0169/93).
P -> A (IN INH-RESISTANT STRAIN
H0948/92).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000763; Bac_ctase/prase
InterPro; IPR002016; Peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfan: PF00141; pcroxidase: 1.
PRINTS, PR00486; PEROXIDASE: 1.
PROXITE: PF00135; PEROXIDASE: 1; 1.
PROXITE: PF00135; PEROXIDASE: 1; 1.
PROXITE: PF00135; PEROXIDASE: 1; 1.
PROXITE: PF00136; PEROXIDASE: 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAGE 10(5593 AAR851671
BAGE 10(5593 AAR851671
BAGE 10(1305 AAR85172 1)
BAGE 10(1305 AAR85172 1)
BAGE 10(1305 AAR85173 1)
BAGE 10(1310 AAR85173 1)
BAGE 10(1311 AAR85173 1)

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                                                                                                                                                                                                                                      SEQUENCE OF 1-94 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; MT1959;
Tuberculist; Rv1908c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
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                                                    STRAIN-H37Rv;
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SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1552 / Oshkosh;
STRAIN-CDC 1552 / Oshkosh;
PRETENSON J., DeBoy R., Dodson R., Oshin M.L., Haft D., Hickey E., PRECLORN J.P., Nelson W. C., Umayam L.A., Ermoleeva M.D., Salzberg S.L., Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gotton S.Y., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Hornsby T., Deylin K., Feltwell T., Gentles S., Hamin N., Hilloy S.,
Hornsby T., Cosborne J., Oualli M.A., Rajadream M.A., Rogers J.,
Rutter S., Gesper K., Skelton S., Squares S., Squares R.,
Sulston J.E., Twylor K., Whitehead S., Barrell B.G.;
Complete ganome sequence.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-H37RV,
MEDIAME-9330010, pubmed-8320241.
HEAD A. Ahang Y., Poulet S., Young D., Cole S.T.;
HEAT STRAINLON Of the katG gene encoding a catalase-peroxidase required for the isonalid susceptibility of Mycobacterium tuberculosis.
                                                                                                               CATA_MYCTU STANDARD;
000129: 000221: 050544; 050546; 050551; 050552; 050553; 050554;
050553; 057215; 057274;
01.-0CT-1994 (Rel. 30; Created)
30-MX-2000 (Rel. 39; Last sequence update)
20-FEB-2003 (Rel. 41; Last annotation update)
Percylalase T (EC 1.111.16) (Catalase-peroxidase T).
KATQ OR RY1908C (R MT1959 OR MTCT180.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 25519;
STRAIN-ATCC 25519;
STRAIN-ATCC 25519;
STRAIN-ATCC 25519;
STRAIN-ATCC 25519;
STRAIN STRAI
                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
Bacteria, Actinobacteride, Actinobacterides
Corynobacterines Mycobacteriaeses Mycobacterium.
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warttila H.J. SOINI H., Huovinen P., Viljanen M.K.;
"kat6 gene mittions in isoniazid-resistant Mycobacterium
tubercollosis strains isolated from Sinnish patients,";
sümmitted (JANN-1996) to the EMEJ/GenBark/DBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION.
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                                                                   RESULT 11
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H0892/92)

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                                                                                                                                                                                                                                                                               Zhang Y., Heym B., Allen B., Young D., Cole S.T.;
"The cortalass-peroxidase gene and isoniazid resistance of
Wycobacterium tuberculosis.";
Nature 358:591-593(1992).
SEQUENCE FROM N.A., AND ISONIAZID RESISTANCE.
                                           MEDLINE-92365822; PubMed-1501713;
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IRON
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MEDLINE-95264910; Pubmed-7746145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGWKSSYGTGTGKDAITSGIEVVWTNTPTKWDNSFLEILYGYEWELTKSPAGAWQYTAKD 357
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                                                                                                                                                                           DB 1; Length 740;
Q -> P (IN INH-RESISTANT STRAIN H0251/90).
                                                                            STRAIN
                                                                                                                                                                     ; Score 2042.5; DB 1; Length
; Pred. No. 1.9e-135;
93; Mismatches 218; Indels
                                                                                                                  -> A (IN REF. 1).
B43C033B533CDDB9 CRC64;
                                   L -> P (IN INH-RESISTANT
15726/89).
                                                                      S -> P (IN INH-RESISTANT H0004/93).
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(Rel. 41, Last annotation update)
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*Missense mutational in the caraisse peroxidase gene, kat6, are
associated with isoniazid realstance in Mycobacterium tuberculosis.";

Mol. Microbiol. 15:353-45(1955).

Mol. Microbiol. 15:353-45(1955).

HONORTON BIRNOLOSIS KAHLEITING BOTH A CATALASE AND
BIRNOL-SPECTRU PEROXIDASE ACTIVITIES. MAY PERA R NOLE IN THE
INTRACELLIAR SURVIVAL OF MYCOBACTERIA (BY SIMILARITY).

-1- CARAIVITIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.

-1- CORACTOR: BIRIS 2 PYCCHORNE IN AND 2 HCORDING PRESIDENT (BY SIMILARITY).

-1- SUBUNIT: HOMOGIMAE (Probbible)

-1- SUBUNIT: HOMOGIMAE (PROBADIAE)

-1- SUBUNIT: BACKONG FOR THE PEROXIDASE FAMILY. BACTERIAL

PEROXIDASE/CATALASE SUBFAMILY.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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ACT_STTE 104 104 BY SIMILARITY.
ACT_STTE 108 108 BY SIMILARITY.
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Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase)
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8231F0FF35397908 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR00216; Percoxidase.
Pfam; PF00141; percoxidase; 1.
PRINTS; PR00458; PEROXIDAS.
TIGRRAMS; TIGR00199; cat_per_HPI: 1.
PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00435; PEROXIDASE_1; 1.
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                                                                                               442 THRDLGPKSRYIGPEVPAEDLIMQDPIPAGNTDYCEEV----VKOKIAQSGLSISEMVST 497
                                                                                                                        416 IHRDMGPVARYLGPLVPKQTLLMQDPVPAVSHDLVGEAEIASIKSQILASGLIVSQLVST 475
                                                                                                                                                            498 AWDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPE-RLAKVLSVYEQI-----SADTG- 550
                                                                                                                                                                                551 --ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFR 608
                                                                                                                                                                                                                                                LGWKSSYGTGTGKDAITSGIEVVWTNTPTKWDNSFLEILYGYEWELTKSPAGAWQYTAKD 357
                                                                                                                                                                                                                                                                                             NWOKKEYVVKPEEMILIDRAQIMGLIGPEMTVLLGGMRVLGINYGGIKHGVFIDCEGQLIN 668
                                                                                                                                                                                                                                                                                                                                                            DFFVNLTDMGNSWK--PVGSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVYAQD 726
                                                      GAGAGTIPDPFGGPG--RSPTMLATDLSLRVDPIYERITRRWLEHPEELADEFAKAWYKL
                               183 -IKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sordariomycetes;
Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Peroxidase/catalase 2 (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
POLINE-2019357; PubMed-12033445;
POTEZZA L., Hansberg W.;
"Neurospora cressa catalases, singlet oxygen and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Fungi, Ascomycota, Pezizomycotina,
Sordarlomycetidae, Sordariales, Sordarlaceae,
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             753 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                115 DAQPKEVQDEVAAWDKVMNLDRFDV 739
                                                                                                                                                                                                                                                                                                                                                                                                                            DNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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PROSITE; PSO0435; PEROXIDASE_1; 1.
PROSITE; PSO0435; PEROXIDASE_2; 1.
PROSITE; PSO0873; PEROXIDASE_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF459787; AAL66352.2; -.
InterPro; IPR002016; Peroxidase.
Pfam: PF00141; peroxidase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiation.";
Biol. chem. 383:569-575(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurospora crassa.
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                                                                                                                                                                                                                        159 SLDKARRILLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDIYW 218
                                                                                                                                                                                                                                                                                 123 SLDKARRLIMPIKQKYGNKISWSDLLLITGNVALESMGKKTFGFAGGRDTWEADESVYW 182
                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                                                                                     EGVNGHPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASD 317
                                                                                                                                                                                                                                                                                                                                                                                                     318 VENQCLGWGNPNWQGKASNAVTSGIEGAWTTNPTKFDWGYFDLLFGYNWELKKSPAGAHH 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 WEPIDIKKENKPV--DASDPSIRHNPIMTDADMAIKVNPTYRAICEREMADPEYFKKTFA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 KAWFKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEE----VVKQKIAQSGLSI 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 SEMVSTAMDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQI----- 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLINDYFVNLLDINTAWK-AADNEGEVFIGYDRKTHDKKWTATRADLIFGAHAELRALAE 711
                                                                                                                                                                   183 GAETTWIG-NEDRYSEGQEGHEGHGVVQGDESKKQHTDIHNRDLQSPLASSHMGLIYVNP
                                                                                                                                                39 KCPVMHGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDFDALKKD
                                                                                                                                                                                                                                                                                                                          GDEKEWLAPSDERY------GDVNKPE----TMENPLAAVQMGLIYVNP
                                            IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
DED01DC6D10BA582 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SADTGASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGFRNWOKKEYVVKPEEMLLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGFRSYGKGTKRVRTEQFLIDRASLLTLSAPELTALIGGLRVLEANYDGSSYGVLTKTPG
                                                                                                                      48;
                                                                                       Length 753;
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
ACT_SITE 87 87 87 BY SIMILARITY.
ACT_SITE 91 91 BY SIMILARITY.
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-3001 (Rel. 41, Last sequence update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                  Matches 382; Conservative 121; Mismatches 199;
                                                                                       49.4%; Score 2003; DB 1; 50.9%; Pred. No. 1.2e-132;
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91 BY
279 IR
83379 MW;
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                                                           753 AA;
                                                                                                      Local Similarity
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              ACT_SITE
ACT_SITE
METAL
                                                         SEQUENCE
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     473 TDY----CEEV--VKQKIAQSGLSISEMVSTAWDSARTYRGSDMRGGANGARIRLAPQNE
                                                                                                                                                                                                    446 VDYKLVDANDIANLKGKILNSGLTTSELVKTAWASASTFRGTDMRGGANGARIRLAPQKD
                                                                                                                                                      WOGNEPERLARVLSVYEQ1-----SAD-TGASIADVIVLAGSVGIEKAAKAAGYDVRV
                                                                                                                                                                                                                                                                                                       PFLKGRGDATAEMTDADSFAPLEPLADGFRNWQKKEYVVKPEEMLLDRAQLMGLTGPEMT
                                                                                                                                                                                                                                                                                                                                                                               566 PFTPGRTDATQGMTDVKSFEVLEPKADGFRNYFDKSNNMSPPEMLVEKASLLKLSVPEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWKPVG--SNAYEIRDRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           626 VLVGGMRVLNANTGQNQYGVFTDKPGTLNNDFFINLLSMSTEWKKSSETEGIYEGYERKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 GAVKWTASRVDLVFGSNSLLRSYAEVYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MASS SPECTROMETRY. MEDLINE-99122365; Pubmed-992496. Gannac-Caffrey V., Hudry-Clergeon G., Petillot Y., Gagnon J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- MASS SPECTROMETRY: MW-81292; MW_ERR-5; METHOD-WALDI.
--- SIMILARITY: BELORGS TO THE PEROXIDASE FAMILY: BACTERIAL
BROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
1-SFB-2003 (Rel. 42, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haloarcula marismortui (Halobacterium marismortui).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730 AA
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InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
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PROSITE: PSO0455; PEROXIDASE_1; 1.
PROSITE: PSO0436; PEROXIDASE_2; 1.
PROSITE: PSSO043; PEROXIDASE_4; 1.
Oxidoreductase; Peroxidase; Iron; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00141; peroxidase; 1. PRINTS; PR00458; PEROXIDASE.
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352
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                                                                                                                                                                                                                                                   24;
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-- SIMILARITY: BELONGS TO THE PEROXIDASE PAMILY. BACTERIAL PEROXIDASE/CAPALASE SUBFAMILY.
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ACT_SITE 104 104 BY SIMILARITY.
ACT_SITE 108 108 BY SIMILARITY.
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19E7931C472973C8 CRC64;
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91; Mismatches 212;
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InterPro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
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                                                                                                                                                                                                                         Amemura-Maekawa J., Watanabe H.;
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108 108 BY
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749 AA; 82914 MW;
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                                    Legionellaceae; Legionella.
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                                                                                                                                                SEQUENCE FROM N.A.
                                                                             NCBI_TaxID=446;
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                                                                                                 36 MSGKCPVMHGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDFDAL 95
                                                                                                               24; Gaps
                                                 DB 1; Length 730;
                                                                           Indels
95 BY SIMILARITY.
258 IRON (HEME AXIAL LIGAND).
81252 MW; 5C7FFFEGC37ADC4B CRC64;
                                               Query Match 49.2%; Score 1998; DB 1; Best Local Similarity 52.7%; Pred No. 2.5e-132; Marches 385; Conservative 103; Mismatches 219;
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95
258 2
730 AA;
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2888711 seqs, 20454813386 residues Scoring table: IDENTITY\_NUC Gapext 1.0 Searched:

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SUMMARIES

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## ALIGNMENTS

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AR098263 2262 bp	Sequence 5 from patent US 6074860. AR098263	AR098263.1 GI:12807520	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 2262)	Robertson, D.E., Sanyal, I. and Adhil	Catalases	Patent: US 6074860-A 5 13-JUN-2000;	Location/Qualifiers
RESULT 1 AR098263 LOCUS	DEFINITION		SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES

961 CAGGGCTTAGGTGGGGCAACCCCAACATGCAGGGCAAGGCAAGCAA	1081 CTGTTCGCTACATTGGGAACTGAAAAGGTCCTGCCGGTGCCCACCATTGGGAACCG 1140 1141 ATGCATCAAAAAGGAAAACAGCCGGTTGCCGACCGCTCTTGGGAACCG 1140 1141 ATGCATCAAAAAGGAAAAAGGCGGTTGAAAAGGAGGAGGAGGAGGAGAGGAGAGGAGAGAGGAG	1141 AFTGACATCAAAAAGGAAACCAGGTFGACGCCAGCGACCCCTCTAFTCGCCAACC 1200 1201 CCGATCAFGACCGATCGGAFAFCGGAFAACCAGACAAACCCAAACCCAACCC	GAAAATTCATGGCCGATCCTGAGTACTTCAAGAAACTTTCGCGAAGGCGTGGTTCAAG 	CTGAGGACCGTGACCTGGCCGCAAAACACGTTAAACGCGCCGGAGGTGCCGGCAAA CTGAGGCGCGTGACCTGGGCCGGAAATCACGTTACATCGGCCGGGAGTGCGGGCGG	1381 GACCTGATTGGCAAACCCGATACGGGAAGAACCGCAATACTGGGAAAAGTGGTC 1440	AAGCAGAAAATTGCACAAAGTGGCCTGAGCATTAGTGAGATGGTCTCCACCGCTTGGGAC 	AGTOCCOGNATTRATOCGOSTTCCGATATGCCCCCCATCTACACTCTCACACTCCCCCCATTCGC	1561 TIGGCCCACACACATGGCCGCACCACCACCACCACCACCCCCACCCCCACCCCACCA	1621   GTTATAGAGATATTCTGCGGATACCGGCGCTACATACCGGTGATACTTGGCCC	1691 GETARGEGRAGGELEGRARANGEGRARAGEGAGGETAGEGGEGTAGTGCCCCTCC 1740		1801 GAGCCGCTGGCCGATGCTTCCGCAACTGCCAAGAAAAAAAA	1861 GAATACCCGCTGATCGTCGCAGCTGGAGGGTAAACGGGCGGG	1921 CAGGGGGTANGGCGCTACTGGGGACCAACTATGGTGGCACCAACACGGGGTATTCACC 1980 1921 CTGGGCGGTANGGCGGTACTGGGCACCAACTATGGTGGACACAAAAGGGGGGTATTCACC 1980	1981 GATTGTGAAGGCCAGTTGACCAACGACTTTTTGTGAACCTGACCGATATGGGGAACAGC 2040 1981 GATTGTGAAGGCAAGTTGAACGAACGACTTTTTGTGAACCTGACGAATATGGGGAAACAC 2040	2041 TGGAAGCCGGTAGCTAGCAACGCCTACGAAATCCGCGACGGCAGGACCGGTGCCGTGAAG 2100
60 G	oy o	a .9. a	oy oy	g g	å 6	Oy Op	o o	oy do	oy op	ç, d	o d	& <del>8</del>	9. 9.	93 D	Oy Db	ò
source 12262 unknown   SE COUNT 553 a 612 c 663 g 434 t   GUELN	ATGANIAGCGARCCGCTGAGATCGACAGAGATGCTTGCAGAGAGATTT 60   ATGANIAGCGATCGCTGAGGATCGATGCTGCAGCAAGAGATTT 60		181 GGGTTGAACCFGGATATTTFCATCAGCAAGATCGCAAATCAGACCCGATGGATCGGAT	09 241 FTCAACTACCGTGAAGAAGTACGGCAACTGCGATTTCGACGCGGTGAAGAAAGA	Oy 301 GCGTTGATGACCAATAGCCAAGAGTGGTGGCCGCTGACTGGGGGGACTACGGCGGTTTG 360 Db 301 GCGTTGATGACCAATAGCCAAAGTGGTGGCCGCTGATGGGGGGGG		421 GGTGGTACCGGAAGCCAGCGCTTGCACGGCTCAACCTGGCGGACAACGTCAGCCTG 480  bb 421 GGTGGTACCGGAAAGCGGTTTGCACCGGTCAACCCTGGCCGAACAACGTCAGCCTTG 480  421 GGTGGTACCGGAAAGCGGTTTGCACCGGTCAACCCTGACCCGAAACGCTGAGCGTTG 480				661 GANANGAGTGGCTGCCTCTGACGAACGCTACGCGAGTGAACAACCAGAGACCAGAAACAGCCAGAAACACCAGAGACGCTGACGAACGCTGACGAACGCTGACGAACGCGAACGCTGAACAACAACAAAACACGAAAAACAGCAAAAACAAAAACAAAAACAAAAAA		781 ANGGGCGACCTGATCGGCTGAGAACCGGACAGGGAGTATTGAAACCTTCGGCGGTTAGAACCTTCGCCGGTTAGAACCTTCGCCGGTTAGAACCTTCGAGAGAGTAGAACTTCGAACTAGAACTAGAACTAGAACTAGAACTAGAACTAGAACTAGAACTAGAACTAGAAAACTAGAAAACTAGAAAACTAGAAAACTAGAAAAAAAA	841 GCGATGAACGAAGAAAAAACCGCAACCCTCAAAGAGCGGCGCGCAACCGTCGGTGGGTAATTGGTAAT	901 CACGGTANTGCCANTGCCTCTGCGCTTAGCCCTGACCCAAAAGCCTCTGACGTTGAAAA	

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vlaAadolocyeopaladalanverialanderea
vlaStasopedereavatlaagecoatilyseessyeesilmereas
Polisfecidotocholangelmereas
ISSSLAT medbyllladecoategoste
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VSIIGTDNEPAARATESLSSYSLPTGELTVGATSL
                                                                                                                                                                                    /LTanslation-"MTIHRINPGTRWSDITVFNGIAHFVEVADSDTSADMQGQVEQVL
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identified by sequence similarity; putative"
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/product transcriptional regulator, Laci family*
/product transcriptional regulator, Laci family*
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/fb.xref="G1:9556064"
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/note-"identified by Glimmer2; putative"
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                                                                                                                  /protein_id="AAF94710.1"
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/gene="VC1558"
complement(8125. .9561)
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/transl_table=11
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//product-giyeout-3-phosphate regulon repressor*
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//protein_id=
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Arpityteriogsaffinessechiarsechiartivquilggrerpstad
Fsglldbellarevarsaqlvrerpydlaadbetytypqqqhrlinygerepyrk
                                                                                                                                                 'note-"similar to SP:P10907 GB:U00039 PID:43249 PID:912455
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TLAOR LVYVROGET BOYOT PREV PURPASSY VALS ESBANNEL PAS, TROGOLIA ROK
TYL LOPONARESEN TIL AI RPEILAS, LEPLAN EEKLD I GVYBELGENGLYHGK I I GOL
ESBODFI AVTREI PLDVHOTLP I WYALBOLHLE POQGKREYGSBRSCTOSSKVASTRO
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NYALYPHMSVYDNLAYGLKNRGVDKQFTAAKTAKVAKTLKIEEYLDRKPAKLSGGGRQ
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PID:606358 GB:U00096; identified by sequence similarity;
                                                                                                                                                                                3B:U00096; Identified by sequence similarity; putative"
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identified by sequence similarity; putative"
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4499. .5260
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/gene="VC1553"
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/gene="VC1554"
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/gene-"VC1554"
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1293. .4474
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10538   TACTGGGGTTCTGAAAAAGAGTGGCTTACCAAATCTGGGGGTGAAAATAGCCGTTACTCT   10597	1189   ATTOGCCACAACCCGATCAGGGATATGGCGATAAAGGTAAATCGGACCTAT   1248

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VVTDLVPTWKTMAGVSTAVTLGSGFVLPVSVPRLPVGLGGLAVRARAVDRACVQRAAA
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LGGRRYVTBCDAVGRSRGLGGNADKFGAPPEMTDKHARAGSR
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VPTAYAELSRYLYLLTDADIRGGKGTAEGAMVESLETRWGPVRVWFGGSTHVRAQFLT
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                                                                                                                              complement(5691, 7025)
/gene-*AGR_L489*
/forte-*probable two-component sensor PA0757 (imported)
Pseudomons seruginosa (strain PA01)*
//codon_start-1
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69.6%; Pred. No. 1.8e-219;
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/db_xref="G1:15158564"
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KTATIVPTPEPSEAGSSKYTSEKORILVSNALDBAILVALGDESTRIAALGOPANHYVR
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LANGIASVILVETLAKUHAELAGITAININIK PTAATETITYNILSYTLIKTOGH
THEIGASVILVEGRAFRENYLLYAQHKCHWSVDDYRADIG ISRDRIGSIIKNATGLSPO
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3738. , 468
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TYAPTILAGYIKTIVARHYGLEARRAYDYKLIBLDLEARLDAYALVALDVSEBALEB
VELESEETIVARHEDAGHGYLIPQHAKOLEKRILLLEBGHCRRQALSFCSTYRAPRY
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/gene-%ARL_484*
3738, .4646
/gene-%ARL_484*
/note-(194335) oxidative stress transcriptional
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complement(4708. 5667)
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1052. .1261
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AUTBORS Wood,D.W., Setubal,J.C., Kaul,R., Wonks,D., Chen,L., Wood,G.E., Chen,Y., Wood,L., Kitejima,J.P., Okuray,N.S., Almeida Jr. N.F., Zhou,Y., Bovee Sr., D., Chapman,P., Clendenning,J. Deatherage,G. Gillet,W., Grant,C., Guenthner,D., Kutyavin,T., Levy,R., Li,M., McClelland,E., Palmieri,A., Raymond,C., Rouse,G., Samphimanchak,C., Wu.Z., Gordon,D., Eisen,J.A., Paulsen,I., Karp,P., Romero,P., Zhang,S., Yoo,H., Tao,Y., Biddie,P., Jung,M., Krespal,W., Perry,W., Gordon-Kamm,B., Lidoo,L., Kim,S., Hendrick,C., and Nester,E.W., Inter Schulssion	Mashington, 1959 NE Pacific Ave, Box 357242, Seattle, Wa 98195-7242, USA 105A 105A Location/Qualifiers  1. 10299 Corganism="Agrobacterium tumefaciens str. C58 (U. Washington)" - genomic DNA* / Strain="C58" (Section 1058)   Section 1058 (Section 1	/db_xref="taxon:180835" 121795 /gene="copR" /gene="synonym: Atu4638" CDS 121755	/gene="cops" /note="identified by sequence similarity; putative; ORF located using Blastx/Gilmmer" /coderted using Blastx/Gilmmer" /coderted using Blastx/Gilmmer" /coderted using Blastx/Gilmmer" /cransl_table=11 /product="two reapment response regulator" /cranslate="two reapment response regulator"	LikEbA*  gene 7922126  /gene="cops" /note="synonym: Atu4639"  CDS 7922126 /gene="cops" /note="identified by sequence similarity; putative; ORF /code teart als Blastx/Gilmmer"	/ Transi Table-II / Product - I-tho. component sensor kinase   / Product - I-tho. III   / Product - II   / Produ	CDS /gene ALUA 040  CDS /gene ALUA 040  /gene 11  /gene 11  /gene 11  /gene 12  /gene 12  /gene 14  /gen

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/gene-MudsGe.
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/gene-MudsGe.
/ote-identified by sequence similarity; putative;
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located using Blastx/Glimmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                   /product="vanillin: NAD oxidoreductase"
/protein_id="AAL45439.1"
/db_xref="GI:17743141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.5%; Score 1098; DB 1;
llarity 69.6%; Pred. No. 1.7e-219;
Conservative 0; Mismatches 650;
                                         note="synonym: Atu4645"
848. .9299
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/transl_table=11
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/gene="vdh"
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Best Local Similarity 69.6%, Pred. No. 41-219;
Matches 1497; Conservative 0; Mismatchos 631; Indels 0;
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                                                                          AGCCCCGAAGAGCTGCTGCTCCTGGGCACACTTCTTGGCCTCACGCGCCGGGAACTC
                                                                                                                                              ACCGTGCTGCTGGGGGGTATGCGGCGTACTGGGCACCAACTATGGTGGCACCAAACACGGC
                                                                                                                                                                         GTATTCACCGATTGTGAAGGCCAGTTGACCAACGACTTTTTTGTGAACCTGACCGATATG
                                                                                                                                                                                                                                                                     GGGAACAGCTGGAAGCCGGTAGGTAGCAACGCCTACGAAATCCGCGAACCGGAAGACCGGT
                                                                                                                                                                                                                                                                                                                                                                    GCCTATTCCTGGGTCCCGACCGCAACAACACTCTATGAGATCCGTGATGGCAAGACCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (18-CCT-1999) Xiuqin Xu, National University of Singapore, Biological Sciences; 10 Science Drive 4, Singapore (Tomail:scip?311@nus.edu.sg, Tel:658743596) Sequence updated (22-CCT-1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H
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Xu,X.O. and Pan,S.O.
An Agrobacterium catalase is a virulence factor involved is timorigenesis
Mol. Microbiol. 35 (2), 407-414 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens kata gene for catalase, AB033631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens (Rhizobium radiobacter)
Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/D_xref="taxon:358"
308. . 4479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGCCTGGACCAAGTGATGAACGCCGACCGTTTCGA 2249
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/db_xref="GI:6691548"
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/gene="katA"
308. .2479
/gene="katA"
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Xu, X.Q. and Pan, S.Q.
Direct Submission
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VERSION
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AUTHORS
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/db_xr
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DALGAACITGEGATAA LEAGALA SILVADI LEAGACHON SILVADI 
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//protein_ld="BACS1952.1"
//protein_ld="ARCS1952.1"
//protein_ld="ARCS1952.1"
//protein_ld="ARCS1952"/"/protein="ARCS1952"/"/protein="ARCS1952"/"/PROTEIN="ARCS19535"/"/PROTEIN="ARCS19535"/
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PPIPPAMKKLIKGAKLKGOKAPATHENEREVERPEDELIGGURFREGERHEVGEKHVVPD
HPOLIKSIKATIKGAKLIKGAKPDHPREGEDWYVARLYMPPLKGDNFFEVETSKITDADDKI
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foote="tph01608"

foote="similar to GB:AAF96702.1 (AE004408) percent

Identity 7 in 656 aa*

foodon_start=1
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identity 81 in 655 aa"
                                                                                                                                                                                                                            /product="putative AraC-type regulatory protein"
/protein_id="BAC61949.1"
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(transl_table=1)
/product-Arp-dependent RNA helicase DeaD*
/db_xref="araCf5]:1.1
/db_xref="61:28608643"
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/transl_table=11
/product="exoribonuclease II"
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/transl_table=11
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/db_xref="GI:28808842"
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/gene=*VPA0609*
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/gene="VPA0608"
6913. .8844
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/profuci-ai-ai-ai-ai-ai-36/1946.1.
/db.zref-97:28808989
/translation-"MKVTWLFKDKVDAISAHQSEFWNWASPTLRDYWSDFLGKAQNSF
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//procein id="Broising"
//proce
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QCKCLYEPIENOVELHHMATLLABQARSRTSPIAKILEDSGTQLMRFYVPASRSEDIR
WIPVRLHSHTLEDLLAELSSDEQACWE
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NORGVYEDWOH HTDPERAVESPE KTI THGELTHALDK LITSOYDARDHE PPAK
LVYNIGALWYRE PI PYRKANNYRAVSTLKKYP ZYKGLEI EREI KVEI EGVRRRGAV
                                                                                                                                                                                                                                                                                                                                               /translation-"MLRESLDMIFNYNLLKPLALLLETKSITATANQMSTSASAVSRT
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identity 72 in 226 aa"
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identity 61 in 272 aa
/codon_start-1
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Identity 37 in 108 aa"
Codon_start-1
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identity 37 in 110 aa"
                                                                                                                            /product-futative transcription activator NahR"
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/db_xref="G1:28808837"
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CCTAGGGAAGATCTGATTTGGCAAGACCCAACGCCAGCAGGCAAAACGGACTACAACGTC 195962 196022 196262 196442 196202 196322 196382 196682 TCGTACGCGGAAGTGTATGCGCAAGATGATAATCAGGAAAATTCATCCATGATTTCGTC 196742 1311 1611 1791 1132 TGGGAACCGATTGACATCAAAAAGGAAAACAAGCCGGTTGACGCCAGCGACCCCTCTATT 1191 TGGTTCAAGCTGACGCACCGTGACCTGGGCCCGAAATCACGTTACATCGGCCCGGAAGTG CCGGCAGAAGACCTGATTTGGCAAGACCCGATTCCGGCAGGTAACACCGACTACTGCGAA 96083 AGAATTCGTTTGGCTCCGCAAAAGATTGGCAAGGTAACGAGCCAGAGCGTCTAAGTCGT 195783 AAGATTICAGAGCGTTICCAACAAGACCCIGCATACTITIGAAGATATGTITGCCCGTGCG GTTCTTGCTGTGCTAGAAAGCATCGCAGCAGAAGAGGGGTGTAGCGTTGCTATC CGCCACAACCCGATCATGACCGATGCGGATATGGCGATAAAGGTAAATCCGACCTATCGC GCTATCTGCGAAAAATTCATGGCCGATCCTGAGTACTTCAAGAAAACTTTCGCGAAGGCG GAAGTGGTCAAGCAGAAAATTGCACAAAGTGGCCTGAGCATTAGTGAGATGGTCTCCACC GCTTGGGACAGTGCCCGTACTTATCGCGGTTCCGATATGCGCGCGGGGGCTAACGGTGCC CGCATTCGCTTGGCCCCACAGAACGAGTGGCAGGGCAACGAGCCGGAGCGCCTGGCGAAA GTGCTGAGCGTCTACGAGCAGATCTCTGCCGACACCGGCGCTAGCATCGCGGACGTGATC GTTCTGGCCGGTAGCCATCGAGAAAGCCGCGGAAAGCAGCTTACGATGTGCGC GITCCCTTCCTGAAAGGCCGTGGCGATGCGACCGCCGAGATGACCGACGCAGACTCCTTC 196263 Greccrireceaeceaegresagecarecreasarargaeseargresarre GTATICACCGATIGIGAAGGCCAGIIGACCAACGACTITITIGIGAACCIGACCGAIAIG 196503 GTCTTTACCGACCGCGGGGTACGTTATCGAACGATTTCTTCGTAAACCTCACGGATATG 96623 CAAGTGAAATGGACGCCGACTCGAGTGGATCTTGTCTTTGGTTCAAACTCGATTCTACGT AAGCCGGAAGAGATGCTGCTGGATCGTGCGCAGCTGATGGGCTTAACCGGCCCGGAAATG ACCGTGCTGCTGGGCGGTATGCGCGTACTGGGCCACCAACTATGGTGGCACCAAACACGGC GGGAACAGCTGGAAGCCGGTAGGTAGCAACGCCTACGAAATCCGCGACCGCAAGACCGGT GCCGTGAAGTGGACCGCCTCGCGGGTGGATCTGGTATTTGGTTCCAACTCGCTACTGCGC TCTTACGCAGAAGTGTACGCCCAGGACGATAACGGCGAGAAGTTCGTCAGAGACTTCGTC

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   CGCGCTGAAGAAGAAGTGTCCACGCTTGATGACCGATAGCCAAGAGTGGTGGCCCGCTGA
                                                                                                        423 TGCGCTCAAGCAAGATTTACAGGCGCTGATGACCGATAGCCAAGACTGGTGGCCGGCAGA
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Engleder, M., Regelsberger, G., Jakopitsch C., Furtmueller, P.G.
Rueker, F., Peschek, G. A. and Obinger, C.
Direct Submission
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EDDVALAGRCKMFEGYSGHPLDPKRAAGEGDDPSQ1RPITLQRGSWIGSNVMIMAGVT
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SIRDSSEELTVHIEKRQGELFAARQALADFONQYSADTPAMQAQHITRLASLKQSIAE
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IT STSYONEPFCILSILEALAAGLYT TPDOGAWARKITDGEBCI YQPNASDLIGK
IELLIASPCHRQRLSRNGFTLAKLYRSDLCYQP I IDSLGGKLTRNYI PLSRTRQKGAL
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                                                                      TEPQESVVHNGVGLPSSSLDTSLKTQLSIPRQAFTFITIGSLIARKGVDRLLKALYLL
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WHPVMNWLVAFWLVVVIGLFFAGNRGVAFGAFSSVYWKIMVMTLAIMMLVTSAKHLNI
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/note="involved in the export of O-antigen and teichoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus tag-"vv12670"
/note="isoleucine patch superfamily; COG0110"
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/protein_id-"AAO11016,1"
/db_xref-"GI:27362161"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"Glycosyltransferase"
/protein_id-"AA011014.1"
/db_xref-"G1:27362159"
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/protein_id="AA011017.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Membrane protein"
/protein_id="RAO11015.1"
/db_xref="GI:27362160"
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/note="COG3307"
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                                                                                                                                                                                                                                                                                                                                                                                     /locus_tag="VV12667"
/note="COG0438"
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6658. .8019
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8136. .8906
                                                                                                                                                                                                                                                                                                    locus_tag-"VV12667"
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/transl_table=11
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Oy 1549 GCCGGCATT Db 111138 GTCGTGTATT OY 1609 AAAGTGCTG Db 111198 AAAGTGCTG OY 1669 ATGGTTCTG OY 1669 ATGGTTCTG OY 1739 AAGTGCTTG	0 1729 GGFTCCC 0 17318 ACGGTTCCC 0 1789 TTCCCACCG Db 111378 TTCCACCGTC 0 1849 GTCAACCCG Db 111438 GTCAACCCTC	Db 111498	REFERENCE 1  ACANAGO SOS APO S
109999 GGCCGTGGTGGTGATACCAGGTTTTGCTCCGTTGAACTCTTGGCCTGAT 110057   469 AACGTCAGCTGGATAACGCGCGTCTGCTGTGGCCGATAGAACAGCGCAAC 528   111   11   11   11   11   11   11	TACTGGGGTGACGAAAAAGAGTGGCTGGCACCTTCTGACGACGCTACGGCGACGTGACTACTGGGGGACGTGACTACTGGGGGACGTACGGCGACGTGCACTACTGGGGGACGTACTGGGGGAAAAAGATGGTTAGGGCCATCTGGTGCAAAAAAAA	TITGECCOTATIGGGATGAAGAGAAAAAAGCGACCOCTAAGAGTIGGGGGGCACACACACACACACACACACACACACACACAC	110778 ATTGCGCACACACACACACACACACACACACACACACACA
8 6 8 6 8	2 8 2 8 2 8 2	8 8 4 8 4 8 6 8 6 8 6	8686868686

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TGCAGGTAATGTGGGTGTTGAGCAAGCCGCAAAGCCGCTGGTATTGCAATC 111317
                                                                                                                                                                                                                                                                                                           1848
                                                                                                                                                                                  GGCCGGTAGCGTAGGCATCGAGAAAGCCGCGAAAGCAGCAGGTTACGATGTG 1728
                                                                                                                                                                                                                                                                                 CTTCCTGAAAGGCCGTGGCGATGCGACCGCCGAGATGACCGACGCAGACTCC 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAGAGATGCTGCTGGATCGTGCGCAGCTGATGGGCTTAACCGGCCCGGAA 1908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCAGAAGTGTACGCCCAGGACGATAACGGCGAGAGTTCGTCAGAGACTTC 2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303450 bp DNA linear BCT 05-MAR-2003 A000032 tious DNA, chromosome 2, complete sequence, 2/6.
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Shinaqawa.H. and Bonda. Vocus phage associated with recent pandemic Vibrio
cyticus associated with recent pandemic Vibrio
cyticus associated with recent pandemic Vibrio
(Acrobiol. 38 (6), 2186-2161 (2000)
TCGCTTGGCCCCACACAACGAGTGGCAGGGCAACGAGCCGGAGCGCCTGGCG 1608
                                                                                       GAGCGTCTACGAGCAGATCTCTGCCGACACCGGCGCTAGCATCGCGGACGTG 1668
                                                                                                                                                                                                                                                                                                                                                                        GCTGGAGCCGCTGGCCGATGGCTTCCGCAACTGGCAGAAGAAGAGTATGTG
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ahaemolyticus
Protoobacteria; Gammaproteobacteria; Vibrionales;
me; Vibrio.
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., Iijima,Y., Najima,M., Nakano,M., Yamashita,A.,
Kimura,S., Yasunaga,T., Honda,T., Shinagawa,H.,
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/ FERRAL TABLE—11

/ PROGUCE—C-CAEALASE

/ PROGUCE—C-CAEALASE

/ PROCEID_C-CAEALASE

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GNNEWVETFPSQGFPIDQNNNSSTFALMANYONKOVFRALLDSSANACLODKROM
ALMGALKREISTAKDLYOARCSPDLRNKALDUKTFPETYGGSBVLKSLJONK"
       /db_xref="G1:28808468"
//drain at.ion="WKIERVAIPTERLEELKGFYEKYFNAVSNDKYHNPKHFSSYFL
SFESGARLELMSNEGVTTGENSHERVPGGAHFAFALGSEQAVDGITKTLVEDGYQRI
OGRRYTGGGYSEGCVLDPDGNRELTV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="macsi646"1"
//db_xaref="si2880846"1"
//translation="%MPRQNEILQLYNDRKRYQYTELSDIIGYSGYTIRODLNFLEDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYLKRYHGAATALQSDD DTRLENREDTKOTLAKRADLYAPNETYLIEGGSANALLA
PRIJAERGDYTITESAY TAHLIRTSANIILLGCYQHQGESLYGPLYRLCIENTHES
TAPLOLDCHQDYGFTSROMMADJARAILAKKRNIYLDDSSKFGOJTPSSTGKYNE
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QGLDGGFYSABOYOGTSNAALLVFYSSDIHATLERYNKFGGOIIRPIFEFFGGCRFH
FYRERGGREAVMSESH
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complement (373 - 408)

/gene="YRA0304"

/gene="YRA0304"

/gene="YRA0304"

/acto="VRA0304"

/acto="VRA0304"

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lodentity 63 in 152 aa"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:AAL20622.1 (AE008775) percent
identity 54 in 243 aa"
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/protein_id="BAC61647.1"
/db_xref="G1:28808470"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence-not_experimental
/transl_table=11
/product="putative regulatory protein"
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/transl_table-11
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/transl_table=11
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/protein_id="BAC61649.1"
/db_xref="G1:28808472"
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/gene="VPA0305"
4319. .5860
/gene="VPA0305"
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/gene="vPA0303"
2974. .3714
/gene="vPA0303"
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/gene="VPA0306"
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/gene="VPA0306"
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                                                                                                                                                                                                                                                                                   (Abases 1 to 303450)
(Abases 1 to 303450)
(Abases 1 to 303450)
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/protain_id="BAGGG4".1"
/db_xef="d1:28808467''
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Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V cholerae
Lancet 361 (9359), 743-749 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"similar to GB:AAA64344.1 (L16865) percent identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome project
Inis clone was isolated from a patient presenting with acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="VPA0300"
/note="similar to EMB:CAC46187.1 (AL591787) percent
identity 68 in 487 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to DBJ:BAB43758.1 (AP003138) percent
identity 57 in 158 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Vibrio parahaemolyticus"
/mol_type="genomic DNA"
/strain="03:K6"
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/protein_id-"BAC61645.1"
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/db_xref="taxon:670"
/chromosome="2"
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/db_xref="G1:28808474"
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67.7%; Pred. No. 1.5e-205;
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                                     /gene="VPA0307"
complement(6548. .7201)
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STRYPRIKORNYR REDVIKLDERALKKILIHATDSOGMARDAGETGGTLRESHIRAG
STRYPRIKORNYR REDVIKLDERALKILIHATDSOGMARDAGETGGTLRESHIRAG
STRYPRIKORNYR REDVIKTORGTSTGTAVANDERALIJAKTROGETSTGTRENDLIJANO
MGLITYNPEGVINGOPDELRENDGTVRTTRGTSTARNIDERAVALIJAGGTTVORKGHRAGHAN
KLIGPRIRARAWETGGGGGATGTAVTTRGTSTARTTBTTGTAVGTSTTLLAYD
WELKRSPAGAMORBETHIKEEDKETVOTEDDA HERPITTROGDAVACHOPTRALLAYD
GLIEDILATORGSAVADTETTAKTRGTSTARTGTORVALAKTTORDPAKACHOPTRALLAYD
AKLASNITTGENVSTANDSRAFTERGSTKGCANGAR HILKPOKORGGRANDDMTDAAK
AKLASNITTGENVSTANDSRAFTERGSTKGCANGAR HILKPOKORGGRANDDMTDASF
DVLLEDILGOTRANDSKAYDTHAGENTERALLAYD
KOVETDBYGALITURGKAYTYR PEELLARGDAGGTATABAR
KARTAROLHGGRAND HILKBERGEN GARAGAGED I UVPRAGGGGDATDMTDASF
DVLLEDILGOTRANDSKAYDTHAGEN TARANTTARANDLYGGLAVLONFTONS
STIRSTRANTAGORNGGRANT TORANDRAGTATABAR
KARTAROLHGGRAND HILKBERGEN GARAGAGED I UVPRAGGGGDATDMTDASF
STIRSTRANTAGTGDVALANTWYRNDREDILA TGGCCAGACTTGATTGTCCTGGCCGGTACTATCGCTTATGAGTCAATGGGACTTAAAACA 1394 ATGGCGATGAACGACAAAAACCGCAGCCCTCACAGCTGGCGGCCACACGTCGGTAAT 118 TGTCCTGTCATGCACGGTGGTAACACCTCGACCGGTACTTCCAACAAGATTGGTGGCCG GAAGGGTTGAACCTGGATATTTTGCATCAGCAAGATCGCAAATCAGACCCGATGGATCCG GATTTCAACTACCGTGAAGAAGTACGCAAGCTCGATTTCGACGCGCTGAAGAAGATGTC CACGCGTTGATGACCGATAGCCAAGAGTGGTGGCCCGCTGACTGGGGGGCACTACGGCGGT TIGATGATCGTATGGCTTGGCACTCCGCTGGCACCTACCGTATTGCTGATGGCCGTGGG 1155 CTAATGATTCGCATGTCCTGGCATGCTGCTTCCTATCGCGTGGCTGATGGGCGTGGC GGCGGTGGTACCGGAAGCCAGCGCTTTGCACCGCTCAACTCCTGGCCGGACAACGTCAGC 1215 GGTGCAGGTACTGGCAATCAGCGTTTCGCTCCATTGAATTCCTGGCCTGACAATGTGAAC CTGGATAAAGCGCCCCTCTGCTGTGGCCGATCAAGAAGAAGTACGGCAACAAAATCAGC TGGGCAGACCTGATGATTCTGGCTGGCACCGTGGCTTATGAGTCCATGGGCTTACCTGCT TACGGCTTCTCTTTCGGCCGCGTCGATATTTGGGAACCCGAAAAAAATATCTACTGGGGT 658 GACGAAAAAGAGTGGCTGGCACCTTCTGACGAACGCTACGGCGACGTGAACAAGCCAGAG 718 ACCATGGAAAACCCGCTGCGCGCTGTCCAAATGGGTCTGATCTATGTGAACCCCGGAAGGT GITAACGGCCACCCIGATCCGCTGAGAACCGCACAGCAGGTACTIGAAACCTICGCCCGI 9; Gaps Length 3865; 45.6%; Score 1030.4; DB 1; Length 68.0%; Pred. No. 2.6e-205; tive 0; Mismatches 676; Indels /product-"catalase-peroxidase KatB" /protein\_id="AAC64361.1" /db\_xref="G1:3764090" Best Local Similarity 68.0 Matches 1455; Conservative 1150 178 1035 298 358 538 598 778 838 238 1095 1335 1566 418 478 Query Match BASE COUNT ORIGIN ö 셤 ò g à g ä 셤 ò g ç g à g ò g ò g ö 셤 à 윱 ö 셤 ò 145826 145765 AAGTACACGTGGGAACCCGTTGGCGAAAACCTTTACGAAATCCGTAGCCGTCGCTCCAAA 145706 145645 GCCTATGCCGAACTGTATGCGCAAGATGACAACGCAGGAAAATTCGTTGAAGACTTTGTC 145586 146065 GTGCCGTTCCTTCCAGGACGTGGCGACACACAGGAGATGACGGATGTTGAGTCTTTC 146006 145766 2151 GTTCCCTTCCTGAAAGGCCGTGGCGATGCGCCGAGATGACCGACGCAGACTCCTTC 1791 BCT 17-0CT-1998 Bandyopadhyay, P. and Stelnman, H.M.
Legionella premomphila catalases peroxidases: cloning of the katB
gene and studies of RatB function
J. Bacteriol. 180 (20), 5369-5374 (1998) 2 (bases 1 to 3865)
Bandyopadhyay, P. and Stelnman, H.M.
Blandyopadhyay, P. and Stelnman, H.M.
Direct 'Dumission
Submitted (14-JUL-1998) Biochemistry, Albert Einstein College of Medicine, 1300 Mortis Park Avenue, New York, NY 10461, USA
Location/Qualifiers ACGGTGCTCGTCGGAGGGATGCGCGTTCTTGGCACAAATCATGGCGGTAGCAAACACGGA 1972 GTATICACCGAITGIGAAGGCCAGIIGACCAACGACTITITIGIGAACCIGACCGAIAIG GATGTAAAATGGACAGCGACCCGCGTCGATCTTGTCTTCGGCTCAAACTCAATACTCAGA 2152 TCTTACGCAGAAGTGTACGCCCAGGACGATAACGCCGAGAAGTTCGTCAGAGACTTCGTC 1792 GCACCGCTGGAGCCGCTGGCCGATGGCTTCCGCAACTGGCAGAAGAAGAGTATGTGGTG **AAGCCGGAAGAGATGCTGCATCGTGCGCAGCTGATGGGCTTAACCGGCCCGGAAATG** GGGAACAGCTGGAAGCCGGTAGCTAGCAACGCCTACGAAATCCGCGACCGCAAGACCGGT GCCGTGAAGTGGACCGCCTCGCGGGTGGATCTGGTATTTGGTTCCAACTCGCTACTGCGC 1912 ACCGTGCTGCTGGGCGGTATGCGCGTACTGGGCACCAACTATGGTGGCACCAAACACGGC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales; Legionellacems; Legionella. 1 (Bases 1 to 3865) AF078110 3865 bp DNA linear BCT 17-C Legionella pneumophila catalase-peroxidase KatB (katB) gene, 145585 GCCGCGTGGACCAAAGTGATGAACGCCGACCATT 145551 /organism="Legionella pneumophila" /mol\_type="genomic DNA" /strain="JR32" 2212 GCCGCCTGGACCAAAGTGATGAACGCCGACCGTTT 2246 /db\_xref-"taxon:446" 882. .3047 882. 3047 /gene="katB" 882. 3047 /gene="katB" /codon\_start=1 /transl\_table=11 Legionella pneumophila Legionella pneumophila AF078110.1 GI:3764089 1. .3865 complete cds. AF078110 1852 2032 145885 2092 145705 1732 SOURCE ORGANISM DEFINITION RESULT 11 AF078110 REFERENCE AUTHORS TITLE MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL gene ACCESSION VERSION KEYWORDS JOURNAL CDS FEATURES

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                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-Mar. 1996) Takesh (Wahmaru, Shituwke University, Bartunke University, Bartunke of Blology, Peculty of Science; 836 Oye, Shituwke, Shituwke 422, Japan (F-mall:sbrush!seci.shituwke ac.jp. Tel:044-238-4702, Far:044-238-0986)

Tel:044-238-4702, Far:044-238-0986)
Sequence updated (12-3-0n-1997).
Location/Qualifiers
                              Synechocystis sp. catalase hpl (katG) gene, complete cds D83990
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                                                                                                                                                                              Bacteria; Cyanobacteria; Chroococcales; Synechocystis
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          linear
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Ushimaru,T., Hayashi,H. and Murata,N.
Nucleotide sequence of katG of Synechocystis:
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65.9%; Pred. No. 1.9e-187;
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/mol_type="genomic DNA"
/strain="PCC 6803"
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/product="catalase hp1"
/protein_id="BAA20459.1"
/db_xref="GI:2198406"
      2896 bp
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/gene="katG"
351. .2615
/gene="katG"
                                                                      D83990.1 GI:2198405
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Ushlmaru,T.
                                                                                                    katG; catalase hpi.
Synechocystis sp.
Synechocystis sp.
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                                                                                                                                                                                               10706 CCGAGTGAAGAGTTGATTTGGCAAGACCCAATCCCGAGCGTCGATTACCGTTTAGTTTGCC
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DQNGTPSGCLIRNBARDOTQNVLHERALITVLVANBRRSVDMODVEELLSMLIGNR
FRACHILLERAGSWUDKYIGDANALIFHGYBARPAET.OLIHAVNRLANATKING
KYELPPLATGYAAVGNYGSGDHPDYTALGDTVNAARLESATKQHHFDLAN
SEKTESYLQDLPQWSATVQOHTLELKGYTNPTTIYGLPPATLGTLUHRSLEDTTPAS
GERTFASIL
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527. .6240
/gene.cyaA.
/note-cyaA.
/codon_start-1
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/note="0RE_ID:slr1992"
/codon_start=1
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/gene="alr1990"
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unknown protein"
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                                                                                                                       Raneko,T., Sato,S., Kotani,H., Tanaka,A., Asamizu,E., Nakamura,T., Huyjima,N., Hirosawa,M., Sugiura,M., Sasamoto,S., Kimira,T., Hosouch,T., Matsuno,A., Muraki,A., Nakazaki,N., Natuo,K., Yasuoda,A., Muraki,A., Nakazaki,N., Natuo,K., Yakaoda,A., Maranabe,A., Yasuda,A., and Tabata,S. Shimada,A., Yasuda,M. and Tabata,S. Shimada,A., Yasuda,M. so yen surain Pcc6603. II. Sequence determination of the entire genome and assignment of potential protein-coding regions 97061201
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PIEELGLVGVREARRSIGTPIERVNAGSYREMKRVAGGLASSDAARARPEPTIKAR
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/protuct-1d-hapfs.'
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//translation-'HRAFETAAVPSOTRIRTORELANTFIKLVPYDNWFREQORIM
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Comp.bemont.1578...2480)
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Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarau, Chiba 292-0812, Japan
(E-mail:tabateRatausa. or. ]p. WHittp://www.kazusa.or.jp/cyano/,
Pai.84.48-52-3933(ex.5330), Rax.81-438-52-3934)
Potential protein coding regions were assigned on the basis of
similarity search of the ORFs and GeneWark analysis.

//organism-Synechocystis sp. PCC 6803*
//orlain-Psynechocystis sp. PCC 6803*
//grain-pcC6803*
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                                                                                                                            /trānslation-"MPLPTSLITTLDGTPLAPBVIADKVVLFVNVASKGGLTPQYSGLV
ALDKAYGEKGLYITVPVONGSAGROEGBERIDFTKTRYDDTLEKQUVNGPNRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A acetyltransferase (thiolase)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGCCGGAAGGGTTGAACCTGGATATTTTGCATCACAAGATCGCAAATCAGACCCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/product="acetyl coenzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"GI:1652965"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALCHGTGGGTAIALERV"
8286. .9008
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8286. .9008
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                                                                                                                                                                                                                                      6955. .8184
/gene="thl"
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                                                                                                                                                                                                                                                                                                                                     /gene-"thl
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Matches 142
                                                                                                                                                                                                                                      gene
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1602 CCTGGCGAAAGTGCTGAGCGTCTACGAGCAGATCTCTGC-----CGACACGGCGCGTAG 1655

=

AATCAGCTGGGCAGACCTGATGATTCTGGCTGGCACCGTGGCTTATGAGTCCATGGGCTT

531

CGTCAGCCTGGATAAAGCGCGCCGTCTGCTGTGGCCGATCAAGAAGAAGTACGGCAACAA

Search completed: October 8, 2003, 12:53:40 Job time : 8212.54 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

8, 2003, 06:24:20; Search time 581.585 Seconds (without alignments) 10459.111 Million cell updates/sec October Run on:

US-09-884-889-5 Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Searched:

5105512 Total number of hits satisfying chosen parameters:

2552756 seqs, 1349719017 residues

Minimum DB seq length: 0 Maximum DB scq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| M. Geneseq\_19Jun03;\*
| California | Califo  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseg/genesegn-embl/NA2002.DAT:\*/SIDS1/gcgdata/geneseg/genesegn-embl/NA2003.DAT:\*

SUMMARIES

		Description	Alcalidenes (Delev	DNA encoding Alcal	Nucleotide sequenc	Sequence encoding	Microscilla furves	DNA encoding Micro	M. tuberculosis ca	Mycobacterium tube
		ID	AAV06554	ABS53944	ABQ78599	AA006815	AAV06555	ABS53945	AAX00818	AAT90400
		DB	19	7	74	11	19	24	20	18
		Match Length DB	2262 100.0 2262 19	2262	2839	2196	2238	2238	2331	2331
-	Query	Match	100.0	100.0	48.5	31.1	29.7	29.7	27.4	27.3
		Score	2262	2262	1098	703	672.2	672.2	620.2	618.6
	Result	NO.	٦	2	e	4	S	9	7	æ

M. tuberculosis ca	Mycobacterium tube	Mycobacterium tube		Mycobacterium tube		(A		Fusarium venenatum	DNA encoding novel	Fragment of Agroba	DNA encoding novel	. Nucleic acid segue	Asperqillus oryzae	Mycobacterium tube	DNA encoding novel	katG gene fragment		gene	katG gene fragment	DNA encoding novel	DNA encoding novel	DNA encoding novel	DNA encoding novel	Oligonucleofide fo	Oligonuclectide fo	katG gene probe #2	DNA sequence of ka	Mycobacterium tube	DNA sequence of ka	σĘ	Mycobacterium tube	Mycobacterium tube	DNA sequence of ka	Mycobacterium tube	Oligonucleotide fo	Oligonucleotide fo
AAX00817	4	AA199683	AA199682	AAT89967	AAT89968	AAQ51531									AAS90138	AAT29130	-	_	- 7				-					_	- 7	-	-			-	-	ABQ23531
50	24	22	22	13	19	14	50	21	23	24	23	21	71	21	23	17	17	17	17	23	23	23	53	24	24	22	19	24	19	19	24	24	19	24	24	54
2331		4403765	4411529	2235																			4653													
27.3	27.3	27.3	27.3	26.8	25.6	25.6	25.6			12.2		6.6						6.0				5.7			4.4	4.2	4.0	4.0						3.9		3.8
618.6	618.6	618.6	618.6	9.909	578.2	578.2	578.2	412.6	299.2	275.6	270.4	224.6	186.4	185.2	170.2	137.2	137.2	135.6	135.6	128.6	128.6	128.6	128.6	98.4	В	ů.	91		σ					87.8	85.2	85.2
σ	10	1	15.	13	14	15	16	11	18	19	20	21	55	53	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	04	7	42	43	44	45
	υ	U	U												U						U	O	O		υ											U

## ALIGNMENTS

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Catalase; epoxidation; hydroxylation; biosensor; paper bleaching;
                                                           Alcaligenes (Deleya) aquamarinus catalase-64CA2 gene.
                                                                                                              Location/Qualifiers
1..2262
/*tag= a
/product= "Catalase-64CA2"
              AAV06554 standard; DNA; 2262 BP
                                            03-JUL-1998 (first entry)
                                                                                               Alcaligenes aquamarinus.
                                                                                 pasteurisation; ss.
                             AAV06554;
RESULT 1
```

97WO-US16513. W09800526-A1. 03-JUL-1997; 08-JAN-1998

Adhikary RS, Robertson DE, Sanyal I; (RECO-) RECOMBINANT BIOCATALYSIS INC 96US-0674887 03-JUL-1996;

**ATGGAAAACCCGCTGGCGGCTGTCCAAATGGGTCTGATCTATGTGAACCCGGAAGGTGTT** 

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or

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The Present sequence is of the Alcolidenes aquamarins cotainse-64CA2 gene. Programmer of the spence and be used to identify related sequences. Catainse-64CA2 may be used to catalyse oxidation reactions such as epoxidation or hydroxylation. The enzyme can also be used to detect or destroy hydrogen peroxide, e.g. in connection with glyoxylic acid production. Nonemores connectic less cleaning puppages to pleaching and partentisation of dary products. Antibodies raised against characterisation of dary products. Antibodies raised against characterisation of deals containing the enzyme.
                                                                              New bacterial catalases, related nucleic acid vectors and transformed cells - used as oxidising agents and for detecting destroying hydrogen peroxide, e.g. in blosensors
                                                                                                                                                                     English
                                                                                                                                                                     Fig 1; 35pp;
                    1998-086953/08
                                        P-PSDB; AAW33809
                                                                                                                                                                     ÷,
                                                                                                                                                                     Claim
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Sequence 2262 BP; 553 A; 612 C; 663 G; 434 T; 0 other;

	ó;	9	9	120	120	180	180	240
	0; Gaps	GCATTT	GCATTI	AAATGT	AAATGT	CCGGAA	CCGGAA	CCGGAT
2262;	ő	GCAGA	GCAGA	GCGGT	GCGGT	GGTGG	GGTGG	TGGAT
100.0%; Score 2262; DB 19; Length 2262;	0; Indels	AGCAAAGAT	AGCAAAGAT	SAGCTATGA	SAGCTATGA	CAAAGATT	ACAAAGATT	AGACCCGA
DB 19;	0;	CCTTCC	CCTTCC	GGGAGA	GGGAGA	CTTCCA	CTTCCA	GCAAAT
2262;	atches	CACAGTA	CACAGTA	GCAATAA	GCAATAA	ACCGGTA	ACCGGTA	CAAGATC
100.0%; Score 2262;	, Mism	CGATCTA	CGATCTA	GCATAGA	GCATAGA	CACCTCC	CACCTCG	GCATCAG
.08;	,	SCTGA	CTGA	CAAG	CAAG	GTAA	GTAA	TTTI
100	ative	PATCC	CATCC	PATCG	PATCG	ACGGTC	ACGGTC	FGGAT
Query Match	Matches 2262; Conservative 0; Mismatches	1 ATGAATAACGCATCCGCTGACGATCTACACAGTAGCTTGCAGCAAAGATGCAGAGCATTT 60	ATGAATAAGGCATCCGCTGACGATCTACAGTAGCTTGCAGCAAAGATGCAGGAGCATTT	61 GTTCCCTTGGTATCGCCAAGGCATAGAGCAATAAGGGAGAGAGCTATGAGGGGTAAATGT 120	61 GITCCCTTGGTATCGCCAAGGCATAGAGCAATAAGGGAGAGCTATGAGGGGTATGAGTATATAGTT 120	121 CCTGTCATGCACGGTGGTAACACCTCGACGGTACTTCCAACAAAGATTGGTGGCCGGAA 180	121 CCTGTCATGGTGGTAACACCTGGGTACTTCCAACAAAGATTGGTGGCGGGAA 180	181 GGGTTGAACCTGGATATTTTGCATCAGCAAGATCGCAAATCAGACCCGATGGATCCGGAT 240
latch	226	1	1	61	61	121	121	181
Query Match	Matches	ογ	Db	οy	qq	οy	qq	٥y

> GGGTTGAACCTGGATATTTTGCATCAGCAAGATCGCAAATCAGACCCGATGGATCCGGAT 181 181

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GAAAAAGAGTGGCTGCCACCTTCTGACGAACGCTACGGCGACGTGAACAAGCCAGAGCC

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1020 1020 1080 1140 1140 1200 1200 1260 1320 1320 1380 1440 1500 1560 AAGCAGAAAATTGCACAAAGTGGCCTGAGCATTAGTGAGATGGTCTCCACCGCTTGGGAC 1500 900 900 960 960 AACGGCCACCCTGATCCGCTGAGAACCGCACAGGTACTTGAAACCTTCGCCCGTATG CTGTTCGGCTACAATTGGGAACTGAAAAAGAGTCCTGCCGGTGCCCACCATTGGGAACCG GAAAATTCATGGCCGATCCTGAGTACTTCAAGAAACTTTCGCGAAGGCGTGGTTCAAG GACCTGATTTGGCAAGACCCGATTCCGGCAGGTAACACCGACTACTGCGAAGAGTGGTC GACCTGATTTGGCAAGACCCGATTCCGGCAGGTAACACCGACTACTGCGAAGAAGTGGTC GGTATCGAAGGTGCTTGGACCACCACCACGAAATTCGATATGGGCTATTTCGACCTG AGTGCCCGTACTTATCGCGGTTCCGATATGCGCGGCGGTGCTAACGGTGCCCGCATTCGC CTGAAAGGCCGTGCCGATGCGACCGCCGAGATGACCGACGCAGACTCCTTCGCACCGCTG GAAAAATTCATGGCCGATCCTGAGTACTTCAAGAAACTTTCGCGAAGGCGTGGTTCAAG CTGACGCACCGTGACCTGGGCCCGAAATCACGTTACATCGGCCCGGGAAGTGCCGGCAGAA TTGGCCCCCACAGAACGAGTGGCAGGGCAACGAGCCGGAGCGCCTGGCGAAAGTGCTGAGC GGTAGCGTAGGCATCGAGAAAGCCGCGAAAGCAGGTTACGATGTGCGCGTTCCCTTC GTCTACGAGCAGATCTCTGCCGACACCGGCGCTAGCATCGCGGGACGTGATCGTTCTGGCC GGTAGCGTAGGCATCGAGAAAGCCGCGAAAGCAGCAGGTTACGATGTGCGCGTTCCCTTC 721 1141 781 781 841 841 901 196 961 1021 1021 1081 1081 1141 1201 1201 1261 1261 1321 1321 1381 1381 1441 1441 1501 1561 1561 1621 1681 901 1501 1621 1681 1741

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This invention relates to the DNA and protein sequences of a novel contribute catalase polypetide. The protein of the invention of its noncious is useful for catalysing the protein of the invention of its noncious is useful for catalysing the breakdown of hydrogen percentage in the protein sequence of the invention is useful for medifying analial molecules. The protein of the invention is analial molecule. The protein of the invention is also useful for catalysing blochemical reactions, for hydrolysing contributed in the protein of the invention is also useful for catalysing blochemical reactions, for hydrolysing specifically to the protein. The nucleace acid sequences of the protein of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTCCCTTGGTATCGCCAAGGCATAGAGCAATAAAGGGAGAGAGCTATGAGCGGTAAATGT
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ilarity 100.0%; Pred. No. 0;
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                                                   Claim 1; Fig 5; 44pp; English.
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Matches 2262; Conserv
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                                                                                                                TGGAAGCCGGTAGGTAGCAACGCCTACGAAATCCGCGGACCGCAAGACCGGTGCCGTGAAG
                                                                                                                                                                                                                                                                                                            GAGCCGCTGGCCGATGGCTTCCGCAACTGGCAGGAAGAAGAGTATGTGGTGAAGCCGGAA
                                                                                             GAGATGCTGCATCGTGCGCAGCTGATGGGCTTAACCGGCCCGGAAATGACCGTGCTG
                                                                                                                                                                                    CTGGGCGGTATGCGCGTACTGGGCACCAACTATGGTGGCACCAAACACGGGGGTATTCACC
                                                                                                                                                                                                                                                                               GATTGTGAAGGCCAGTTGACCAACGACTTTTTTGTGAACCTGACCGGATATGGGGAACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene; ss; marine bacteria; catalase; hydrogen peroxide; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAMAGTGATGAACGCCGACCGTTTCGACGTCGCGTCGTAA 2262
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/product= "Catalase protein"
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990S-0412347
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1881   GGTAGCGTAGGCATCGAGAAAGCCGCGAAAGCAGCTTACGATCCCTTC   1740     1741   CTGAAAGCCGTGGCGATGCGACCGCGAAAGCAGCTTACCTTCCGCCGTTCCCTTC   1800     1741   CTGAAAGCCGTGGCGATGCGACCGCGAGATGACCGAGACTCCTTCGCACCGCT   1800     1741   CTGAAAGCCGTGGCGATGCGACCGCAGAACACACTCCTTCGCACCGCT   1800     1801   GAGCCGTGGCCGATGGCTTCCGCCAGATGACAGACACACTCTTCGCACCGCA   1800     1801   GAGCCGTGGCCGATGGCCAACTGCCAGAAAAGAAACATGCCTGCAGAA   1800     1801   GAGTTCCTGGCAACTGGCCAACTGCCAACAACACCGCCTGAATGACCGGAA   1800     1801   GAGTTCTGGCATCTGCCCAACTGACGAACAACACCGCCTGCTTG   1920     1801   GAGTTCTGCACTTCTGCCAACTTACGCCTTAACCGGCCCGAAATGACCTGCTGCTG   1920     1801   GAGTTCTGCACTTATGGCAACTTACGCCTGCAATGACCCGCAATTCACC   1800     1801   GAGTTGTGCACTTATGGCACCAACTTATGACCGGCAATTCACC   1800     1801   GATTGTGAAGCCCAGTTATGGCAACTTATGACCAGAATGACCAGCACTATCACC   1800     1801   GATTGTGAAGCCCAACTTATGACTACCTGCACAATGACCAGCACTATCACC   1800     1801   GATTGTGAAGCCCAACTACCAACTTATTGTGAACCCGCAATTGACCGCTGTAACCGCCTATTCACC   1800     1801   GATTGTGAAGCCCAACTACCAACTTATTTTGAACCTGCAATTGACCGCTGAACC   2100     1801   GGAAGCCGGTACGTGACCAACTTTTTTTGAACCTGCAATTGGGGAACACCCCTGAACCCCTGTAACCGCCTTAACCGCTTAACCGCCTTAACCGCTTAACCTTAACCGCTTAACCGCTTAACCGCTTAACCGCTTAACCGCTTAACCACCACCACACCACCACACCACACCACCACACACCACCACA	Db
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Determining the ability of a compound to remove a reactive oxygen species (ROS), useful in pharmaceutical and nutraceutical Itelds ameasuring activities of antioxidants, comprises providing a cell having ROS-inducible promoter

Disclosure; Page 56-63; 70pp; English

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The present sequence encodes Agrobacterium tumefaciens catalase (KatA). KatA has a promoter which is induced by a reactive oxygen species (ROS). The KatA gene can be used in the method of the invention. The specification describes method for determining the ability of a compound to remove a ROS. The method comprises providing a cell having a ROS-inducible promoter operably linked to a reporter gene that is heterologous to the promoter, and exposing the cell to a compound protentially able to remove the ROS. The method is useful in determining the ability of a compound or gene product to remove a ROS and determining the lovel of the ROS HOZ inside a cell, to properly assess and label anticidant products for uses as ROS supplements, natural products or drugs. The method may also be used in selecting for new or improved ROS drugs. scavengers

Sequence 2839 BP; 580 A; 854 C; 843 G; 562 T; 0 other;

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Best Local Similarity 69.6%;
Matches 1488; Conservative 112 452 292 512 572 412 652 712 332 172 232 352 172 g g g 셤 g 셤 ò 셤 ò ò q 윱

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                                                                                                                                                                                                                                                                                                                         258 AGTACGCAAGCTCGATTTCGACGCGCTGAAGAAGATGTCCACGCGTTGATGACCGATAG 317
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                                                                                                                                                                                            CCAAGAGTGGTGGCCCGCTGACTGGGGGCACTACGGCGGTTTGATGATCCGTATGGCTTG 377
                                                                                                                                                                                                                                                   498 GCTGTGGCCGATCAAGAAGAAGTACGGCAACAAAATCAGCTGGGCAGACCTGATGATTCT 557
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                                TTTGCATCAGCAAGATCGCAAATCAGACCCGATGGATCCGGGATTTCAACTACCGTGAAGA
                                                                                                                                                              180 GTTTCAAAAACTAGACTATTGGGCGCTCAAAGAAGATTTGCGCAAACTGATGACGGAAAG
                                                                                                                                                                                                                                                                                                           GCGCTTTGCACCGCTCAACTCCTGGCCGGACAACGTCAGCCTGGATAAAGCGCCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  599 CTCT-----GAACGCTATTCCGGTGATCGCGA------CCTCGAAAACCCGCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTGTCCAAATGGGTCTGATCTATGTGAACCCGGAAGGTGTTAACGGCCACCCTGATCC
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2152 TCTTACGCAGAAGTGTACGCCCAGGACGATAACGGCGAGAAGTTCGTCAGAGACTTCGTC 2211
                                                                                                                                                                                                                                                                             2132 ACCGTCCTCATCGCGGCCTCGCGCGTCATCGCGCCCAATTACGGCGGTCGCGCGCATGGC
                                                                                                                                                                2252 GCCTATTCCTGGGTCCCGACCGGCAACATCTCTATGAGATCCGTGATCGCAAGACCGGC
                                                                                    1972 GTATTCACCGATTGTGAAGGCCAGTTGACCAACGACTTTTTTGTGAACCTGACCGATATG
                                                                                                                2192 GICTICACCGATAAGCCGGGGGCGCTTACAACGGACTTCTTCACGACGTTGACGGACATG
                                                                                                                                                                                                       GCCGTGAAGTGGACCGCCTCGCGGGTGGATCTGGTATTTGGTTCCAACTCGCTACTGCGC
                                                                                                                                                                                                                                 2312 GCAGCCAGATATTCGGCAACCCGCGTCGATCTCGTGATCGGCTCCAACTCCAATCTGCGC
                            1912 ACCGTGCTGCTGCGCGCTATGCGCGTACTGGGCACTATGGTGGTGGCACCAAACACGGC
                                                                                                                                              GGGAACAGCTGGAAGCCGGTAGGTAGCAACGCCTACGAAATCCGCGAACCCGCTACGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contg. genetic information of heat resistant peroxidase - pd. by culturing transformant and collecting heat resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 31.1%; Score 703; DB 11; Length 2196; Best Local Statilarity 62.1%; Pred. No. 3.2e-189. Matches 1326; Conservative 0; Mismatches 765; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence may be used to construct plasmid poD10 used to tran
E.coll UW258. The transformed expression system may be used
produce heat resistant peroxidase in large quantities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2196 BP; 576 A; 564 C; 633 G; 423 T; 0 other;
                                                                                                                                                                                                                                                                                                                     Sequence encoding heat resistant peroxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89JP-0089469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        poD10; E.coli UM228; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-372008/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-1990
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150 CGGTACTTCCAACAAGATTGGTGGCCGGAAGGGTTGAACCTGGATATTTTGCATCAGCA 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 CGATTTCGACGCGCTGAAGAAGATGTCCACGCGTTGATGACCGATAGCCAAGAGTGGTG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Present sequence is of the Microsculla furvascens cotalises-530Al gene. Programmers of the gene can be used to identify related sequences. Outsides-530Al may be used to catalyse oxidation reactions such as epoxidation or hydroxylation. The empressmen can also be used to detect or proxidation or hydroxylation. The empressmen can also be used to detect or production insertion with glyosyllo acid production processing the proxided and pasternism of dairy products. Antibodies raised against catalises 530Al can be used to soreen libraries for detection and purification of cells conteaning the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCGCTGACTGGGGGCACTACGGCGGTTTGATGATCCGTATGGCTTGGCACTCCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 AGATCGCAAATCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 AGAICTGGCAGCGGTIAAAAAGGACCTGGCAGCGCTAATGACAGATTCACAGGACTGGTG
                                                                                                                                                                                                   Catalase; epoxidation; hydroxylation; biosensor; paper bleaching;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New bacterial catalases, related nucleic acid vectors and
transformed cells used as oxidising agents and for detecting
destroying hydrogen poroxide, e.g. in biosensors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 2238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quory Match 29.7%; Score 672.2; DB 19; Best Local Similarity 59.5%; Pred No. 1.9e-180; Best Local Similarity 6); Mismatches 1277; Conservative 0; Mismatches 808;
                                                                                                                                                              Microscilla furvescens catalase-53CA1 gene.
                                                                                                                                                                                                                                                                                                                                                                     "Catalase-53CA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                                                                                                                                                                                                                         Location/Qualiflers
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                                          AAV06555 standard; DNA; 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0674887.
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                                                                                                                                                                                                                                                                 Microscilla furvescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-086953/08.
                                                                                                                                                                                                                             pasteurisation; ss.
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                                                                                                                         03-JUL-1998
                                                                                  AAV06555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1922 TGGGCGGTATGCGCGTACTGGGCACCAACTATGGTGGCACCAAACACGGGGGTATTCACCG 1981
GGATATGGCGATAAAGGTAAATCCGACCTATCGCGCTATCTGCGAAAAATTCATGGCCGA 1277
                                                                                                                                                                                  1833 TIGGCGGTTTGCGCGTGTTGGGC-CGAACTATCGGCATCTGCCTCATGGCGTCTTCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACGGCGGCCCGGGTGGTCTCATTTTCGGATTTTACGCCCAAGACGACAACCAAGAAG
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                                                                                                                                                                                                                                           1398 CCCGATTCCGCCAGGTAACACCGACTACTGCGAA-----GAAGTGGTCAAGCAGAA
                                                                                                                                                                                                                                                                                  1299 TCCGATTCCAGAAGTCGATTACGAATTGACAGAAGCGGAAATTGAAGAAATCAAAGCCAA
                                                                                                                                                                                                                                                                                                                       1449 AATTGCACAAAGTGGCCTGAGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCG
                                                                                                                                                                                                                                                                                                                                                    1509 TACTTATCGCGGTTCCGATATGCGCGGCGGTGCTAACGGTGCCCGCATTCGCTTGGCCCC
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                                                                            1278 TCCTGAGTACTTCAAGAAACTTTCGCGAAGGCGTGGTTCAAGCTGACGCACCGTGACCT
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        339 CACCTACCGTATCGGTGATGGCCGTGGTGGCGGTGGCTCCGGCTCACAGCGCTTCGCGCC 398
                                                                     450 GCTCAACTCCTGGCCGGACAACGTCAGCCTGGATAAAGCGCGCCGTCTGCTGTTGGCCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to the DNA and protein sequences of a novel to purified cratalsee polypeptide. The protein of the invention or its homologue is useful for catalysing the breakdown of hydrogen peroxide. The protein sequence of the invention is useful for modifying amail in molecules, by mixing the protein of the sequence of the invention is useful or modified small molecule. The protein of the invention is also useful for catalysing blochemical reactions, for hydrolysing also also useful for catalysing blochemical reactions, for hydrolysing of prosidic linkages and for generating antibodies which bind specifically to the protein. The nucleic acid sequences of the capture is useful as a probe to determine whether a biological ample, out an organism having the nucleic acid or out as a soil sample, contains an organism having the nucleic acid or cauch as a soil sample, contains an organism having the nucleic acid or capture for invention is useful in immunoffinity chosency repression in a biological sample. The callulase protein of the contains a protein of the protein of the invention is useful in immunoffinity chosency repression in a biological sample. The callulase protein of the contains and regain activity after exposure to temperatures of from chosen and regain activity after exposure to temperatures of from chosen and the present sequence concerns of the contains protein of the forwart of the present sequence concerns of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.9e-180;
0; Mismatches 808;
     /product= "Catalase protein"
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97US-0951844.
99US-0412347.
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Best Local Similarity 59.5%;
Matches 1277; Conservative (
                                                                                                                        19-JUN-2001; 2001US-0884889
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(ADHI/) ADHIKARI R.
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                                        US2002102680-A1
                                                                                                                                                                                                                                                                                                                                    Robertson DE,
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05-OCT-1999;
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variation WO9850585-A1.	PF 06-MAY-1998; 98WO-US092885.  XX XX XX AMAY-1997; 97US-0852219.  XX XX YX XX	CC The invention realists to a novel method of detecting wyCobacterium cc tuberculosis. The method comprises amplifying the DNA in the samples to CC generate a detectable amount of amplified DNA comprised actalases cc memorial of the comprises are submitted DNA fragment has a serie to comprise a train #1778 MC kat6 gene sequence. The method optionally comprises determining if the kat6 MN fragment has a serie to comprise a determining if the kat6 MN fragment has a serie to threonine mutation in coden 313 (\$3157 mutation), indicative of an controlline mutation in coden 313 (\$3157 mutation), indicative of an controlline mutation in coden 313 (\$3157 mutation), indicative of an earlied can be used to detect W. tuberculosis in this disease is composed in the best of the ethod can be used to detect MI stands to the ethodical fluids. CC and subsequent treatment depends on identification of the ethodic agent CC MR tuberculosis truth has been used in tuberculosis treatment, but controlline and subsequence is not provided in the specification; it has been cc created by modifying the katg gene sequence given in Fig 7.  Sequence 2331 BP; 455 A; 735 C; 762 G; 379 T; 0 other:	Query Match   27.4%;   Score 620.2;   DB 20;   Length 2331;   Best Local Similarity   Si.7%;   Pred.   Mo. 1.254-165;   Match 1234;   Conservative   O;   Mismetches   Bi8;   Indels   Si. Caps   Bi9;   Match 1234;   Conservative   O;   Mismetches   Bi8;   Indels   Si. Caps   Bi9;   Discourage   Discour
1515 TCGCGGTTCCGATATGCGCGCGGGTGCTAACGGTCCCGCATTCGCTTGGCCCCACAGAA   1	1584   CCAGGAGGATTTAACCAGGCAATCAGATAACAAACCAGGATATCGTTGGCCGACCTGAT   1643     1671   CGTTCTGCGGATAGGATAGAAAACCAGGAAAACAGCAGGTTACGATGGG   1710     1644   TGTGCTGGCGGATGGGATGGAAAAACCGCGAAAAAAACGCCAGAAAAAACTGCTGCCCTTAGGTGA   1701     1644   TGTGCTGGCGGTGGCGGGGGTGTAAAAAAAAACTGCTGCCCTTAGGTGA   1703     1731   CGTTCCCTTCCTGAAAGGCCGTGGCGAAAAAAACGCCGAAAAAAACGCCGAAAAAAAA	1911 GACCGTGCTGGGGGGTATGCGCGTACTGGGGACCAACTATGGGGGCCCCAACTACGGG 1970     1914 GACGTTTGGTAGGGGGTATGCGGGTACTGGGGACCAACTACGAGGGTTCGCAACTGGGGTTCGCAACTGGGGTTCGCAACTGGGTTCGCAACTGGGTTCGCAACTGGGTTGGTT	0y 2205 CTFGGTGGCCGCCGGACCAAGTGAAGGCGGCGCGTTGGA 2219  Db 2184 TTTGGAAGGCCTGGGCCAAGCTAAGTGGACCGGTTTGA 2228  RESULT 7  AAXO0818  XX  CAXO0818;  XX  CAXO0819;  XX  AXO0819;  XX  XX  CAXO0819;  XX  XX  XX  XX  XX  CAXO0819;  XX  XX  XX  XX  XX  XX  XX  XX  XX

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GCAAGCAACGCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAAACCCCACGAAATTC 1059
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                                     GCGCTGAAGAAGATGTCCACGCGTTGATGACCGATAGCCAAGAGTGGTGGCCGCCTGAC
                                                                     TGGGGGCACTACGGCGGTTTGATGATCCGTATGGCTTGGCACTCCGCTGGCACCTACCGT
                                                                                                                        TACGGCCACTACGGGCCGCTGTTATCCGGATGGCGTGGCACGCTGCCGGCACCTACCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCAGGACTGGTGGCCCAACCGGCTCAATCTGAAGGTACTGCACCAAAACCCGGCCGTC 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA sequence comprises a consensus of the Mycobacterium tuberculosis wild-type kafe (catalabse percaidase) gene. Claimed methods of rapidly identifying strains of M. tuberculosis which are resistent to the tuberculostatic duty isonizatid (INN) are based on the discovery of 4 mutations in the wild-type gene sequence that conform INN resistance and which coincidently result in the addition or deletion of restriction endouchease sites. Primars (see ANT90401-02) are provided for the PCR amplification of the katG gene of a test strain of M. tuberculosis, and future primars (see ANT90403-06) for use in the restriction framement sea manification defined manification described an analysis of the smallfic gene of manification framements.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining susceptibility of Mycobacterium tuberculosis strains to isoniazid - by detecting mutation(s) in the catalase-peroxide gene,
                                                                                                                                                                                                                                                                                                                        G to T transversion at base 1457 alters codon 463 from CGG (Argo) to CTG (Leu) leading to isoniald resistance, and eliminates a Ncil-MspI restriction site*
                                                                                                                                                                                                                               A to G transversion at base 1079 alters codon 337 from TAC (Tyr) to TGC (Cys) leading to isoniazid resistance, and
                                                                                                                               G to C transversion at base 1013 alters codon 315 from AGC (Ser) to ACC (Thr) leading to isoniazid resistance, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 618.6; DB 18; Length 2331; Pred. No. 3.4e-165;
                                 G to C transversion at base 859 alters codon 264 from GCG (Ala) to ACG (Thr) leading to isoniazid resistance, and
                                                                                                                                                                                  produces a new MspI restriction site"
                                                                                  a CfoI restriction site"
                                                                                                                                                                                                                                                                              eliminates a Rsal restriction site"
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Mismatches 819;
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Best Local Similarity
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INH; diagnosis; detection; ss.
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Matches 1253; Conservative
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                                                                                                                                                                               1591 AACGACCCCGACGGGGATCTGCGCAAGGTCATTCGCACCCTGGAAGAGATCCAGGAGTCA 1650
                                                                                                                                                                                                                                                                                                                      GGTAGCGTAGGCATCGAGAAAGCCGCGAAAGCAGCTTACGATGTGCGCGTTCCCTTC 1740
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                                                            GACTACTGCGAAGAAGTGG------TCAAGCAGAAATTGCACAAAGTGGCCTG
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          GGCCCGGAAGTGCCGGCAGAAGACCTGATTTGGCAAGACCCGATTCCGGCAGGTAACACC
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The invention realtes to a novel method of detecting Mycobacterium to the invention realtes to a novel method of detecting Mycobacterium continuerculosis. The method comprises amplifying the DNA in the samples to generate a detectable amount of amplified DNA comprising a catalase.

DE PROVIDE (RIGHO) NA fragment with sequence of bases 904-153 of the PNA tuberculosis strain H378v MC ketG gene sequence. The method optionally contriber comprises determining if the ketG DNA fragment has a serine to threonine mutation in codon 315 (8315T mutation), indicative of an controlled and hydratide (INNI) reselstant Mr tuberculosis strain. The method can be used to detect M. tuberculosis in biological fulids, controlled on be used to detect M. tuberculosis. This disease is a major cause of human morbidity and mortality, and conclusive disposas in the disease treatment depends on identification of the etiologic agent M. tuberculosis. Rim is many of method conclusive disposas in the disposal strains have emerged; the method allows such drug-resistant strains have emerged; the method allows such drug-resistant extrains to be identified. The present sequence represents the wild-type M. tuberculosis kind one of the etiologic agent M. tuberculosis kind one of the conclusive disposation when the defendence represents the wild-type M. tuberculosis kind one of the conclusive disposation when the defendence represents the wild-type many tuberculosis.
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                                                                                                         Catalase-peroxide; katG; isonicotinic acid hydrazide; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.3%; Score 618.6; DB 20; Length 2331; 58.7%; Pred. No. 3.4e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of Mycobacterium tuberculosis - by amplifying kat6 and detecting specific fragment, and optionally identifying INN-reasistant strains by detecting specific mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product- "catalase peroxide"
/note- "the start codon is not indicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
M. tuberculosis catalase peroxide (katG) gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2331 BP; 455 A; 734 C; 763 G; 379 T; 0 other;
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0; Mismatches 819;
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
70..2292
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39634 GAGGCTGCTCCGCTGGAGCAGATGGGCTTGGGCTGGAAGAGCTCGTATGGCACCGGAACC 39575
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                                                                                                                                                                                                                                               CCGATCTATGAGCGGATCACGCGTCGCTGGCTGGAACACCCCGGAGGAATTGGCCGACGAG
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                                                                                                                                             760 TATGTGAACCCGGAAGGTGTTAACGGCCACCCTGATCCGCTGAGAACCGCACAGCAGGTA
                                                                                                                                                                GGCCACACCGTCGGTAATTGTCACGGTAATGGCAATGCCTCTGCGTTAGCCCCTGACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39217 GGGCCGCTGGTCCCCAAGCAGACCTGCTGTGGCAGGATCCGGTCCCTGCGGTCAGCCAC
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                                                              GACGTGAACAAGCCAGAGACCATGGAAAACCCGCTGGCGGCTGTCCAAATGGGTCTGATC
                                                                                                                                                                                                                            820 CTTGAAACCTTCGCCCGTATGGCGATGAACGACGAAAAAACCGCAGCCCTCACAGCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a noval method for identifying essential genes for survival or the method comprises aligning the ground relates of mycohetteria species. The method comprises aligning the ground response of a second mycohetterian species of my expense of a second mycohetterian species and selecting a genomic sequence of a second mycohetterian species and selecting a counterpract in other bacterial sequences and that corresponse to conserved in both genomes with no connection from the survival or virilence of mycohetterian species and that corresponds species species from the survival or virilence of mycohetterian for the survival or virilence of mycohetterian for the invention is useful for detecting My. Understalling the trapers and protective mycohetterial diseases, particularly tubervilosis and injury. The present sequence the survival diseases, particularly Mycohetterial consisting the sequence used in the method of the Invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 TCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCTCGATTTCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618.6; DB 24; Length 82993;
                                                                                                                                                                                                                                                                                 Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences Mycobacterium tuberculosis and W. leprae -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 82993 BP; 14881 A; 26628 C; 26719 G; 14765 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 4; 874pp; English
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58.7%;
                                                                            22-FEB-2002; 2002WO-IB01973
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W0200274903-A2.
                                       26-SEP-2002
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Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                      monitoring.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPro at segdata.uspto.gov/sequence.html?DocID=6294328B1.
                                     The invention relates to evaluating strain variation within and between different populations of the tuberculosis betreatial partitions. Mycobacterium tuberculosis or related wycobacterium by determining the mucleotide agequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the mucleotide agequences of w. tuberculosis strains CDF 151 (MN1968) and HN78 (MN1968). The method isrundings strains CDF 151 (MN1968) and w. tuberculosis and has valuable application in the fields of tuberculosis and has valuable application to the fields of tuberculosis.
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     Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 819;
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Pred. No. 1.2e-163;
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Matches 1253; Conservative
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                                                                   18797 ACCCCGGGCCGCACGGATGCGTCGCACGAACAACCGACGTGGAATCCTTTGCCGTGCTG
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1981 GATTGTGAAGGCCAGTTGAACGACTTTTTGTGAACCTGACCGATATGGGGAACAGC 2040	RESULT 12 AA199682/C ID AA199682 standard; DNA; 4411529 BP. XX AC AA199682; XX AC AA199682; DY 15-JAN-2002 (first entry)	Mycobacterium t Mycobacterium t Variation; epid Mycobacterium t US6294328-B1.	PF 24-JUN-1998; 98US-0103840. XX XX XX XX XY Fleischmann RD, White OR, Fraser CM, Venter JC; XX XX XX Y Fleischmann RD, White OR, Fraser CM, Venter JC; XX XX XX Y Fleischmann RD, White OR, Fraser CM, Venter JC; XX XX XX XX XY Freischmann RD, White OR, Fraser CM, Venter JC; XX XY XY Y Freischmann RD, White OR, Fraser CM, Venter JC; XY Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y	
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TGGACCAAAGTGATGAACGCCGACCGTTTCGACGT 2252 = = = = = 1300 1240 1360 1420 1468 1588 1861 2041 2098 2158 2218 2155005 2154948 2154888 2154828 2154768 2154708 2154648 2154588 1637 1681 2154468 1741 1801 2154348 1921 2154108 2154048 2153988 g g g à g g ò 셤 g q g a g 셤 셤 g à à à à ò å a à à ç 5 ç ð ö 셤 ŏ ŏ 셤 õ GCCCTGACGCGGGACATCGAGGAAGTGATGACCACCTCGCAGCCGTGGTGGCCCGCCGAC 2155828 2155708 2155477 2155306 2155126 2155066 GCAAGCAACGCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAACCCCACGAAATTC 1059 GACCCCTCTATTCGCCACAACCCGATCATGACCGATGCGGATATGGCGGATAAAGGTAAAT 1239 339 459 579 759 939 AACAAAGATTGGTGGCCGGAAGGGTTGAACCTGGATATTTTGCATCAGCAAGATCGCAAA 219 TCCATGGGCTTACCTGCTTACGGCTTCTTTCGGCCGCGTCGATATTTGGGAACCCGAA 639 -ATGAGGTCTATTGGGGCAAGGAAGCACTGGCTGG-----GCGATGAGGGTTACAGC GCGCTGAAGAAAGATGTCCACGCGTTGATGACCGATAGCCAAGAGTGGTGGCCCGCTGAC TGGGGGCACTACGGCGGTTTGATGATCCGTATGGCTTGGCACTCCGCTGGCACCTACCGT ATTCCTGATGGCCGTGGGGCGGTGGTACCGGAAGCCAGCGCTTTGCACCGCTCAACTCC TGGCCGGACAACGTCAGCCTGGATAAAGCGCGCCGTCTGCTGTGGCCGATCAAGAAGAAG TACGGCAAGAAGCTCTCATGGCCGGACCTGATTGTTTTCGCCGGCAACTGCGCGCTGGAA GACGTGAACAAGCCAGAGACCATGGAAAACCCGCTGGCGGCTGTCCAAATGGGTCTGATC GGTAAGCGGGATC-----TGGAGAACCCGCTGCCGCGCGCTGCAGATGGGGCTGATC TATGTGAACCCGGAAGGTGTTAACGGCCACCCTGATCCGCTGAGAACCGCACAGGTA CTTGAAACCTTCGCCCGTATGGCGATGAACGACGAAAAAACCGCAGCCCTCACAGCTGGC CGCGAGACGTTTCGGCGCATGGCCATGAACGACGTCGAAACAGCGGCGCTGATCGTCGCGC GGCCACACCGTCGGTAATTGTCACGGTAATGGCAATGCCTCTGCGTTAGCCCCTGACCCA AAAGCCTCTGACGTTGAAAACCAGGGCTTAGGTTGGGGCAACCCCAACATGCAGGGCAAG 2155245 GAGGCTGCTCCGCTGGAGCAGATGGGCTTGGGCTGGAAGAGCTCGTATGGCACCGGAACC GGTAAGGACGCGATCACCAGCGCATCGAGGTCGTATGGACGAACACCCCGACGAAATGG GATATGGGCTATTTCGACCTGCTGTTCGGCTACAATTGGGAACTGAAAAAGAGTCCTGCC 2155125 GACAACAGTTTCCTCGAGATCCTGTACGGCTACGAGTGGGAGCTGACGAAGAGCCCTGCT GGTGCCCACCATTGGGAACCGATTGACATCAAAAAGGAAAACAAGCCGGTTGACGCCAGC 2155065 GGGGCTTGGCAATACACGCCAAGGACGGCGCGGTGCCGGCACCATCCCGGACCGTTC TCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCTCGATTTCGAC AAAGATATCTACTGGGGTGACGAAAAAGAGTGGCTGGCACCTTCTGACGAACGCTACGGC Length 4411529; Indels DB '22; Score 618.6; DB 22; Pred. No. 1.2e-163; O; Mismatches 819; Similarity 58.7%; 3; Conservative Best Local Sim Matches 1253; 160 2156007 280 2155887 340 2155827 00 2155767 460 2155707 640 200 2155476 260 2155425 820 2155365 880 2155305 940 1155185 1180 1120 Query Match à g à 윱 õ 셤 ò a à g à 셤 à g ð 셤 à g ò g ò g ò 셤 õ 셤 à 셤 ö 셤 ð 윱 셤 ò ô

2154949 2154769 2154829 2154589 2154349 2154169 2153929 2154529 2154229 2154109 1636 1740 1467 GGCGGCC---AGGCGCTCCCCGACGATGCTGGCACTGACCTCTCGCTGCGGGGTGGAT CTGAAAGGCCGTGGCGATGCGACCGCCGAGATGACCGACGCAGACTCCTTCGCACCGCTG AACGACCCCGACGGGGATCTGCCAAGGTCATTGGCACCCTGGAAGAGATCCAGGAGTCA 2154528 TTCAACTCCGCGGCGCGCGGGAACATCAAAGTGTCCTTCGCCGACCTCGTCGTGCTCGGG GAGATCCTCCTCGATCGTCCGCAGCTGATGGCTTAACCGGCCCGGAAATGACCGTGCTG 2154288 TACATGCTGCTCGACAAGGCGAACCTGCTTACGCTCAGTGCCCCTGAGATGACGGTGCTG CCGACCTATCGCGCTATCTGCGAAAATTCATGGCCGATCCTGAGTACTTCAAGAAAACT TTCGCGAAGGCGTGGTTCAAGCTGACGCACCGTGACCTGGGCCCCGAAATCACGTTACATC GGCCCGGAAGTGCCGGCAGAAGACCTGATTTGGCAAGACCCGATTCCGGCAGGTAACACC GACTACTGCGAAGAAGTGG-------TCAAGCAGAAAATTGCACAAAAGTGGCCTG AGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCGTACTTATCGCGGTTCCGAT AACGAGCCGGA---GCGCCTGGCGAAAGTGCTGAGGGTCTACGAGCAGATCT-----------CTGCCGACACGGCGCGTAGCATCGCGGACGTGATCGTTCTGGCC GGTAGCGTAGGCATCGAGAAAGCCGCGAAAGCAGCAGGTTACGATGTGCGCGTTCCCTTC 2154408 ACCCCGGGCCGCACGGATGCGTCGCAGGAACAAACCGACGTGGAATCCTTTGCCGTGCTG CTGGGCGGTATGCGCGTACTGGGCACCAACTATGGTGGCACCAAACACGGCGTATTCACC 2154228 GTAGGTGGCCTGCGCGTCCTCGGCGCAAACTACAAGCGCTTTACCGCTGGCGTGTTCACC 1981 GATTGTGAAGGCCAGTTGACCAACGACTTTTTTTGTGAACCTGACCGATATGGGGAACAGC 2154168 GAGGCTCCGAGTCACTGACGACTTCTTGGTGAACGTGCTGGATATCACC TGGAAGC----CGGTAGGTAGCAACGCCTACGAAATCCGCGACCGCAAGACCGGTGCCGTG AAGTGGACCGGCAGCCGCGTGCTCTTCGGGTCCAACTCGGAGTTGCGGGCGCTT **AAGTGGACCGCCTCGCGGGTGGATCTGGTATTTGGTTCCAACTCGCTACTGCGCTCTTAC** GCAGAAGTGTACGCCCAGGACGATAACGGCGAGAAGTTCGTCAGAGACTTCGTCGCCGCC

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     292 TACGGCCACTACGGGCCGCTGTTTATCCGGATGGCGTGGCACGCTGCCGGCACCTACCGC
                                                           760 TATGTGAACCCGGAAGGTGTTAACGGCCACCCTGATCCGCTGAGAACCGCACAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1114 GGCGGGCC---AGGGCGCTCCCCGACGATGCTGGCCACTGACCTCTCGCTGCGGGTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1171 CCGATCTATGAGCGGATCACGCGTCGCTGGCTGGAACACCCCGGAGGAATTGGCCGACGAG
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                                      400 ATTGCTGATGCCGTGGGGGGGGGGTGTACCGGAAGCCAGCGCTTTGCACCGCTCAACTCC
                                                                                                               TGGCCGGACAACGTCAGCCTGGATAAAGCGCGGCCGTCTGCTGTGGCCGATCAAGAAGAAG
                                                                                                                                                                                                                                                                                                                                          AAAGATATCTACTGGGGTGACGAAAAAGAGTGGCTGGCACCTTCTGACGAACGCTACGGC
                                                                                                                                                                                                                                                                                                                                                                           590 -ATGAGGTCTATTGGGGCAAGGAAGCCACCTGGCTCG-----GCGATGAGCGTTACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       643 GGTAAGCGGGATC----TGGAGAACCCGCTGGCCGCGGTGCAGATGGGGCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    820 CTTGAAACCTTCGCCCGTATGGCGATGAACGACGAAAAAACCGCAGCCCTCACAGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1060 GATATGGGCTATTTCGACCTGCTGTTCGGCTACAATTGGGAACTGAAAAAGAGTCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1120 GGTGCCCACCATTGGGAACCGATTGACATCAAAAAGGAAAACAAGCCGGTTGACGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1240 CCGACCTATCGCGCTATCTGCGAAAATTCATGGCCGATCCTGAGTACTTCAAGAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1360 GGCCCGGAAGTGCCGGCAGAAGACCTGATTTGGCAAGACCCGATTCCGGCAGGTAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1420 GACTACTGCGAAGAAGTGG------TCAAGCAGAAAATTGCACAAAAGTGGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 TCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCTCGATTTCGAC 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This partial DNA sequence encodes the katG gene of Mycobacterium tuberculosis strain #378 which is used in a novel method for repidly tuberculosis strain #378 which is used in a novel method for repidly form. I sonicotinic each Mycratide; The method involves the use of restriction fragment length polymorphism (RFLP) analysis to determine if a NcII-MSPI restriction site is absent in the DNA of the strain at the codon corresponding to codon 463 for M. tuberculosis AstG gene comsensus sequence (see ANWIJ343). The absence of the site indicates an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGACCCGATGGGTGCGGGTTCGACTATGCCGCGGAGGTCGCGACCATCGACGTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determination of isoniazid sensitivity of Mycobacterium tuberculosis strains - by restriction length polymorphism analysis of katG gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 606.6; DB 19; Length
Pred. No. 8.6e-162;
0; Mismatches 819; Indels_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2235 BP; 431 A; 696 C; 745 G; 363 T; 0 other;
2153928 TGGGACAAGGTGATGAACCTCGACAGGTTCGACGT 2153894
                                                                                                                                                                                                                                         katG gene; isoniazid resistance; INH; acid hydrazide; ss.
                                                                                                                                                                                                        Mycobacterium tuberculosis partial katG gene
                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "katG gene
/note= "partial cds"
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                                                                                          AAT89967 standard; DNA; 2235
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st Local Similarity 58.6%;
tches 1252; Conservative
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                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                         Tuberculosis;
isonicotinic a
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                                                                                                                                                                 20-MAR-1998
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                                                                                                                            AAT89967;
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This partial DNA sequence encodes the katG gene from a variant strain of Mycobactrium tuberculosis H3TAV which is used in a novel method to rapidly identify strains of M. tuberculosis which are resistent to isoniazed (INM, also known as isoniconting cald hydrazide). The method involves the use of restriction fragment length polymorphism (FREP) analysis to determine if a NcIr-MspI restriction site is absent in the DNA of the strain at the codon corresponding to codon 463 of a M. tuberculogis watG gene consensus sequence (see MW3143); the absence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 AACAAAGATTGGTGGCCGGAAGGGTTGAACCTGGATATTTTGCATCAGCAAGATCGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19; Length 2221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.6%; Score 578.2; DB 19; Length ilarity 57.8%; Pred. No. 1e-153; Conservative 0; Mismatches 838; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2221 BP; 432 A; 691 C; 735 G; 363 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculogis katu geme commun....of the site indicates an INH-resistant strain.
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Column 12-14; 18pp; English.
                                  /*tag- a
/product- "katG gene"
/note- "partial cds"
Cocation/Qualiflers
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Matches 1229; Conserva
                                                                                                                                                                                                                                                                                                                     WPI; 1998-007975/01.
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                                                                                                                                                                              18-APR-1994;
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                               AACGACCCCGACGGGGATCTGCGCAAGGTCATTCGCACCCTGGAAGAGATCCAGGAGTCA
                                                                                                                                                                                                                               1681 GGTAGCGTAGGCATCGAGAAAGCGGGAAAGCAGGATTACGATGTGCGCGTTCCCTTC
                                                                                                                                                                                                                                                                                                                                                                      1741 CTGAAAGGCCGTGGCGATGCGACCGCCGAGATGACCGACGCAGGCTCCTTCGCACCGCTG
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            AGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCGTACTTATCGCGGTTCCGAT
                                                                                 ATGCGCGGCGGTGCTAACGGTGCCCGCATTCGCTTGGCCCCACAGAACGAGTGGCAGGGC
                                                                                                                                                     1588 AACGAGCCGGA---GCGCCTGGCGAAAGTGCTGAGCGTCTACGAGCAGATCT-----
                                                                                                                                                                                                                                                                                                                                                                                                         1711 ACCCCGGGCCGCACGGATGCGTCGCAGGAACAAACCGACGTGGAATCCTTTGCCGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2010 TGGGAGCCCTCGCCAGCAGGATGACGGACCTACCAGGGCAAGGATGGCAGTGCCAAGGTG
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isoniazid; INH; katG; ss. catalase-peroxidase; isonicotinic acid hydrazide; antibiotic; susceptibility; sensitive; resistant;

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                                                                                                                                                                                                                                                                                                                                                 The kntG gene of Mycobertellum tuberculosis was isolated on a KpnI fragment by shotgun cloning the sequence contains one open reading fragment by shotgun cloning the sequence contains one open reading frame with high coding probability, a 735 mains acid protein is encoded by the offer having predicted mall.w. 18039. This protein encoded by the offer having predicted mall.w. 18039. This protein encoding to the structure of Known backetain catalase peroxidases which consist of two modules (possibly the result of a diplication event), both showing homology to the yeast enzyme, fissed to a unique the knick gene can result in loss of INH-susceptibility, i.e. the formation of a Table formation of a Table formation of a Contract protein a firsting the formation of a STARA-2003 to correct PM field.)
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                                                                                                                                                                                                                                                    isoniazid, rifampicin or streptomycin resistance in tuberculosis
by detecting mutation in katG, rpoB or rpsL genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 4795;
                                                                                                                                                                                                                                Rapid detection of antibiotic resistance in Mycobacteria - esp
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57.8%; Pred. No. 1.5
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                                        UNIV BERNE.
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Matches 1229; Conservative
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Zhang Y;
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US-09-884-889-5 2262 Perfect score:

IDENTITY\_NUC Scoring table: Sequence:

1731049 seqs, 1297405648 residues Gapop 10.0 , Gapext 1.0 Searched: .

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ALIGNMENTS

Sequence 5, Application US/09884889 Patent No. US20020102680A1 GENERAL INFORMATION:

NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin version 3.0 SEQ ID NO 5 LENGTH: 2262

; ORGANISM: Alcaligenes (Deleya) aquamarinus US-09-884-889-5 DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 29.7%; Score 672.2; DB 10; Length 2238; Best Local Similarity 59.5%; Pered. No. 1.38-199; Matches 1777; Conservative 0; Mismatches 808; Indels 60;
                                                                                                                                                                                                                                                                        CURREMY PALCATION WROBER: US/09/084,889
CURREMY FILING DAME: 2001-06-19
PRIOR PAPLICATION WINDER: US 08/412,347
PRIOR PAPLICATION WINDER: US 08/951,844
PRIOR FILING DAME: 1999-10-05
PRIOR FILING DAME: 1999-10-10
PRIOR FILING DAME: 1997-10-10
PRIOR PLING DAME: 1996-00-03
WHORN FILING DAME: 1996-00-03
Sequence 7, Application US/09884889
Patent No. US20020102680A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Microscilla furvescens
US-09-884-889-7
                                                           REREAL, INCROMENTOR
APPLICANT. DIVERSA CORPORATION
APPLICANT. SANFAL. INGUELL
APPLICANT. SANFAL. INGUELL
APPLICANT. ADMIRARI. ROBERT
APPLICANT. ADMIRARIANT
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APP
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Page 4

40156 ATCCACGACACCGGGGGGGGGGGGGGGGGGGGGTGCGGTTGGGCCGCTTAACAGG 40 TGGCCGACACGCGGGGGGGGGGGGGGGGGGGGGGGGGGG		39754   CGCGGGGCGCGGCATGGCCATGGAGGGCGCGCGGGCGCGTGATCGTCGGG   3964   GGCGACGCGGTGGTATTGTCACGGTATGGAGGGCGCGCTGGTCGGGCGGCGGGCG	1180 GACCCCTATTGCCACAACCGATCATCACCGGATATGCCGATAAAGGTAAT   1
	6 6 6 6 6	8 3 8 3 8 3 8 3 8 3 8	
1811 GAAGCCGGAAGATGCTCCTGGATCCTCCCTGACCTCATACCGGCCTGGAAAT 1910	2004 CAACACTAANTGCGAGCCACGATGATAACTATTTTAAGCGAGAGATTTCAA 2063   2085 GACCGGTGCGTGAAGTGCACCCCGGGGGTGATTTTAAGCGAGAGATTTCAA 2063   2084 AATGCCGAAGTAAGTGGACCCCGGGGTGACTTGCTATTTGCATTCTACATCAT	RESULT 3  19.0-080-170-645/c  19.0-080-170-645/c	Query Match         27.3%; Score 618.6; DB 15; Length 82993;           Bost Local Similarity         58.7%; Pred. No. 3.2e-181;           Matches 1253; Conservative         0. Mismatches 819; Indels 63; Gaps 8;           160 AACAAGATGGTGGCGGAAGGTGAACTGGAATTTTGCATCACAGCAAGTGCGAA         219           110 AACAAGATGGTGGCCGAACGGTCAACTGGAATTTTGCATCACCAGCAAGTGCGCAA         219           10 AACAAGATGGTGGCCGAACGGTCAACTGGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTCAACTAATTTGAATTTGAATTTGAATTTGAATTTAATTA

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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                    ATTORNEY ACRET INFORMATION:
NAME: CARROLL, PETER G.
REGESTRATION NUMBER: 32, 817
REFERENCE/DOCKET NUMBER: PORS-01756
TELECOMMUNICATION INFORMATION:
TELECAN (413) 397-8384
INFORMATION FOR SEQ ID NO. 144:
SEQUENCE CHARACTERISTICS:
                                                                        APPLICATION NUMBER: US/09/940,925A FILING DATE: 10-Jun-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLEUDE TYPE: DNA (Genomic) STOURNCE DESCRIPTION: SEQ ID NO: 144: US-09-940-925A-144
           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                  LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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19037 AAGCGCGGCGGCCCAACGTGGTCGCTTGTCGCCTGCACCACAAGTGGGGTGGAAGTC 38978
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                                                                                                                                                                   8917 TTCAACTCCGCGGCGCCGGGGAACATCAAAGTGTCCTTCGCCGACCTCGTCGTGCTCGGT 38858
                                                                        1588 AACGAGCCGGA---GCGCCTGGCGAAAGTGCTGAGCGTCTACGAGCAGATCT----- 1636
                                                                                                                                      ------CTGCCGACACCGGCGCTAGCATCGCGGACGTGGTCGTTCTGGCC 1680
                                                                                                                                                                                                    GGTAGCGTAGGCATCGAGAAGCCGCGAAAGCAGCAGGTTACGATGTGCGCGTTCCCTTC 1740
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                                                                                                                                                                                                                                                                                                                    136 CCTGCTGGCGCTTGGCAATACACCGCCAAGGACGGCGCCGGTGCCGGCACCATCCCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                     1462 GGCCTGAGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCGTACTTATCGCGGT
                                                Gaps
                                             15;
   DB 11; Length
                                             Indels
Query Match 6.1%; Score 137.2; DB 11; Best Local Similarity 54.3%; Pred. No. 4.7e-32; Matches 330; Conservative 0; Mismatches 265;
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APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAYLD M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

PATHOGENS

Sequence 144, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:

US-09-940-925A-144

RESULT 4

STREET: 220 MONTGOMERY STREET, SUITE CITY: SAN FRANCISCO STATE: CALIFORNIA

CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL

NUMBER OF SEQUENCES: 165

COUNTRY: UNITED STATES OF AMERICA ZIP: 94104

COMPUTER READABLE FORM:

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TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 148:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 620 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        994 GGCAAGCCAAGCCAACGCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCCAACCCCACG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1054 AAATTCGATATGGGCTATTTCGACCTGCTGCTTCGGCTACAATTGGGAACTGAAAAAGAGT 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1174 GCCAGCGACCCCTCTATTCGCCACCACCCGATCATGACCGATGCGGGATATGGCGATAAAG 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1234 GTAAATCCGACCTATCGCGCTATCTGCGAAAATTCATGGCCGATCCTGAGTACTTCAAG 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1294 ANAACTTTCGCGAAGGCGTGGTTCAAGCTGACGCACCGTGACCTGGGCCCCGAAATCACGT 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 AAATGGGACAACAGTTTCCTCGAGATCCTGTACGGCTACGAGTGGGAGCTGACGAAGAGC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 CCTGCTGCCGCTTGGCAATACACCGCCAAGGACGGCGGCGGGTGCCGGCACCATCCCGGAC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 ccerrcecceccc---aescecrccccahcenscreccarcarcarcarcarcarcarcacae 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGAGTTCGCCAAGGCCTGGTACAAGCTGATCCACCGAGACATGGGTCCCGTTGCGAGA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GGAACCGGTAAGGACGCGATCACCACCGGCATCGACGTATGGACGAACACCCCGACG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 137.2; DB 11; Length 620;
Pred. No. 4.7e-32;
0; Mismatches 263; Indels 15;
                                                                                      APPLICANT: BROW, MARY ANN D.
LIAMACHEV, YICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                     TIP: 9110
COMPUTER READABLE PORM:
REDILIN TYRE: ROPPY disk
COMPUTER: TAR FO COMPUTER:
COMPUTER: TAR FO COMPUTER:
SOFTWARE STERM: PC-DOS/MS-DOS
CURRENT AFPLICATION DAYR:
RPILICATION UNDER: US/09/940,925A
FLING DARE: 10-Jun-2002
FLING DARE: 10-Jun-2002
ATPORNEY: AGENT INFORMATION:
                                                                                                                                                                                                NUMBER OF SEQUENCES: 155
CORRESCONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL
STREET: 220 MONTGOMENT STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-940-925A-146
                  Sequence 146, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 54.3%;
Matches 330; Conservative (
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US-09-940-925A-146
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1354 TACATCGGCCCGGAAGTGCCGGCAGAAGACCTGATTTGGCAAGACCCGATTCCGGCAGGT 1413
                                                                                                                   1414 AACACCGACTACTGCGAAGAAGTGG~~~~~~~~TCAAGCAGAAAATTGCACAAAGT 1461
                                                                                                                                                                                                                                                                                                                                                                  1522 TCCGATATGCGCGGCGGTGCTAACGGTGCCCGCATTCGCTTGGCCCCACACAACGAGGTGG 1581
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                                                                                                                                                                                                                                                                                                                                                                                                                      553 AGGACAAGGGGGGGGGGCAACGGTGGTGGTGCGCTGCTGCAACGCCACAAGTCGGGTGG 612
                                                       373 TACCTIGGGCGCTGGTCCCCAAGCAGACCTGCTGTGGCAGGATCCGGTCCTTGCGGTC 432
                                                                                                                                                                               433 AGCCACGACCTCGTCGGCGAAGCCGAGATTGCCAGCCTTAAGAGCCCAGATCCTGGCATCG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1462 GGCCTGAGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCGTACTTATCGCGGT
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLIVE, DAVID M. ...
TITLE OF INVENTION: RAPID DESCRION AND IDENTIFICATION OF PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Owery Match 6.1%; Score 137.2; DB 11; Length Best Local Similarity 54.3%; Pred. No. 4.76–13. Matches 33; Conservative 0; Mismatches 263; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUPTRY: UNITED STATES OF AMERICA
27P: 94104
KENINY TIPE: Floppy disk
COMPUTER: TBM FC COMPUTER: TBM FC COMPUTER:
OPERATING SYSTER: PC-COMPARE:
OPERATING SYSTER: PC-COMPARE:
SOCTHARR: PSTCHTIN FELONO #1.0, VETSION #1.30
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ADDRESSEE: MEDLEN & CARROLL
STREET: 220 WONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CARGOLI, PETER 6.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/940,925A FILING DATE: 10-Jun-2002 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 148:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 148, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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TELEPHONE: (415) 705-8410  THORMATION FOR SEQ ID NO: 130: SEQUENCE CHRANGTELSTICS: TYPE: INCECTELSTICS: TYPE: INCECTE CALLA TYPE: INCECTE CALLA MOLECULE TYPE: DNA (9enomic) SEQUENCE DESCRIPTION: SEQ ID NO: 150: US-09-940-9254-150	Query Match 6.1%; Score 137.2; DB 11; Length 620; Best Local Similarity 54.3%; Pred. No. 4.7e-32; Matches 330; Conservative 0; Mismatches 263; Indels 15; Gaps 2;	994 GGCAAGCAACCACGTACCACCTCGGGTATCGAAGGTCTTGGAACCCCACCACCCCAC 1053	OY 1054 AAATTCGAFAIGGCTATICGACCTGCTGGTTCGGCTACAATTGGGAACTGAAAAAGAGT 1113	0y 1114 CCTGCCGGTGCCCACATTGGGAACCGATGACAAAAAGAAAG	Oy 1174 GCCAGGACCCCTATTCGCCACAACCGATCATGACGATGAGGGATATGCCGATAAG 1233	9y 1234 GTARATCOGACCTATGGGGGAAAAATTCATGGCGATGCTGAGTACTTCAAG 1293  B	Oy 1294 AAAACTITGGGGAGGGTGGTTCAAGCTGACGCACGGACCTGGCCCGAAATCACGT 1353	03   1354   TACATCGGCCCGGAAGTGCCGGCAGAAGACCCGATTCCGCCAGGT 1413   1   1   1   1   1   1   1   1   1	dy 1414 aacaccactactacaadaadtag	Qy 1462 GGCCTGAGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCGTACTTATCGCGGT 1521  120 Anti-	0y 1522 TCCGARANGGGGGGGGGTGCTAGCGGGARTCGCTTGGCCCCACAGAACGAGTG 1581  Db 68 AGCCACAACGCGGGGGGCACAACGGTGGTCAACCGAACGCAACGCACACGCACCAACGGGGGG 9	Oy 1582 CAGGGAA 1589 b	RESULT B US-09-041-1934-144  Sequence 144, Application US/09941193A   Sequence 144
1054   AARTICGATATGGACTGCTGCTGTGGGCTACAATTGGGAACTGAAAAAGGT	QY 1234 GTAAATCCGACCTATCGCGCAAAAATTCATGGCGGATCCTGAGTACTTCAAG 1293	OY 1294 AANACTITCGCGAAAGGCGTGGTTCAAGCTGACGCACCGTGACCTGGGCCCGAAATCACGT 1353 Db 308 GACGACTCGCCAAGCCCGTRCAAGCTGATCAACGGAACAGGGGTCCCGTGGGGACACGGGACAACGGGTCCCGTAAAAATGGAACAAAAAAAA	9y 1354 TACATCGGCCCGGAAGTGCCGGCAGAGACCCGATTCCGGCAGGT 1413	Oy 1414 AACACCGACTACTGCGAAGAGTGGTCAAGCAGAAATTGCACAAGT 1461 Db 188 AGCAGAGCTGGCTGAGCGGAATTGCCAGCTTAAAAGCCAATCCGGGAATG 129	0y 1462 GGCCTGAGCATAGTGAGTGCTCCACCGCTTGGGACAGTGCCCGTACTTATGGCGGT 1521  Db 128 GGATTGACTGCTCACAGTAGTTGCACCGAACGGAGGGGGGGG	Oy 1522 TCCGATATCCGCGCGCGCTGCTAACGGTGCCCGCATTCGCTTGCCTCACAGAACGAGTGG 1581  Db 68 AGGACAACGCGCGCCCCAACGGTGCTCCACTCGCCTCCACCACACGTCGGTGG 9	Oy 1582 CAGGGCAA 1589 Db 8 GAGTCAA 1	RESULT 7 US-09-940-925A-150/c	Sequence Lob, Application US/U940925A   Publication No. US20030054338A1   GENERAL INFORMATION: APPLICANT: RESENCE NARY ANN D.		NORRESTON TO THE CARNOLL STATE TO STATE	GITY: ALL PRANCISCO STATE: CALLEDED STATES OF AMERICA COUNTY UNITED STATES OF AMERICA Z.ZP. 94104	COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IRM PC COMPACTAL  COMPUTER: IRM PC COMPACTAL  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: PATENTIN MOREN: 05/09/40,925A  FULNO TORRENT OFFE: 10-700 - 2002  CLASSIFICATION MOREN: 05/09/40,925A  ATTORNEY/AGRET INFORMATION:  NAME: CARROLL, PETER G.  REGISTRATION NUMBER: 32,837  REPERRENT NUMBER: 13,837  TELECOMMUNICATION INFORMATION:

us-09-884-889-5.rnpb

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994 GGCAAGGCAAGCAACGCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAACCCCACG 1053
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   553 AGGACAAGGGGGGGGGGGGCAAAGGGTGGTGGCATCGCCTGCAGCACAAAGTCGGGTGG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1054 AAATTCGATATGGGCTATTTCGACCTGCTGTTCGGCTACAATTGGGAACTGAAAAGAGT 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGTTCGCCGGCC---AGGCGCTCCCCGACGATGCTGGCCGCCACTGACCTCTCGCTGCGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GGAACCGGTAAGGACGCGATCACCACCGGCATCGAGGTCGTATGGACGAACACCCCGACG 75
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILIM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARR: PEREDETIR Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
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54.3%; Pred. No. 4.7e-32;
+1ve 0; Mismatches 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CARROL, PETER G.
REGISTRATION NUMBER: 3, 837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECHONER: (415) 705-8410
INPORMATION FOR SED ID NO: 146:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/941,193A FILING DATE: 28-Aug-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 146:
                                                                                                                                                                                                                                                                  US/09941193A
                                                                                                                                                                                                                                                                                                                                                                 VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHOGENS
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   OLIVE, DAVID M.
                                                                                                                                                                                                                                                       Sequence 146, Application US/0994; Publication No. US20030108973A1; GENERAL THFORMATION: APPLICANT: BROW, MARY ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: SAN FRANCISCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                 LYAMICHEV,
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                                                                                 1582 CAGGGCAA 1589
                                                                                                                                  613 GAGGTCAA 620
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 620;
                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MAS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 137,2; DB 11;
Pred. No. 4.7e-32;
0; Mismatches 263;
                                                                                                                                                                                                                                                                                                                                                                            ATTORNET/AGENT INFORMATION:
NAME: CARROLL, FPIRE 6.
REGISTRATION NUMBER: 32,837
REPRENEMCE/DOCKET NUMBER: PORS-01756
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION WHORER: 18/09/941,193A
FILING DATE: 28-Aug-2001
CLASSIFICATION: <unknown>
                                                                                               COUNTRY: UNITED STATES OF AMERICA
2 IP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genonic)
SEQUENCE DESCRIPTION: SEQ ID NO: 144:
US-09-941-193A-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 705-8410
TELEPAX: (415) 997-8338
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 620 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                    COMPUTER READABLE FORM:
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Best Local Similarity 54.34
Matches 330; Conservative
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994 GGCAAGGCAAGCAACGCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAACCCAACG 1053
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                                                                                                                                                                                                                                                                                                                                                                425 CCGTTCGGCGGCCC---AGGGCGCTCCCCGACGATGCTGGCCACTGACCTCTCGCTGCGG
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                                                                                                     1114 CCTGCCGGTGCCCACCATTGGGAACCGATTGACATCAAAAAAGGAAAACAAGCCGGTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
         4.7e-32;
                           0; Mismatches
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      No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 150, Application US/09941193A Publication No. US20030108873A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
         Pred.
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      54.3%;
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COMPUTER READABLE FORM:
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                           330; Conservative
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      Best Local Similarity
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                           Matches
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313 GACGAGTICGCCAAGGCCTGGTACAAGCTGATCCACCGAGACATGGGTCCCGTTGCGAGA 372
                                                                                                                                                                              433 AGCCACGACCTCGTCGGCGAAGCCGAGATTGCCAGCCTTAAGAGCCAGATCCTGGCATCG 492
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WEDION TYPE: ROLOPY disk

WEDION TYPE: TOPOPY disk

COMPUTER: IN PC COMPAILIBLE

COMPUTER: IN PC COMPAILIBLE

COMPUTER: TO-TOS/ANS-DOS

SOFTANRE: PATENTIAL PC-TOS/ANTA-

CONFRINT APPLICATION NUMBER: US/O9/941,193A

RILING DATE: 28 4 mg - 2001

CLASSIFICATION: GIRKOWN->

ATTORNEY/AGETI INFORMATION:
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TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CARROLL, PETER C,
REGISTRATION WOMBER: 20, 337
REFERENCE/COCKET NUMBER: PORS-01756
TELECOMOUNICATION INFORMATION:
TELEPRONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UNITED STATES OF AMERICA
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 148:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 148, Application US/09941193A
Publication No. US20030108873A1
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEC ID NO: 148:
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STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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APPLICATION NUMBER: US/09/941,193A

Score 137.2; DB 11; Length 620;

6.18;

Query Match

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994 GGCAAGGCAAGCAACGCCGTGACCTCGGGTATCGAAGGTGCTTGGACCAACCCCAACCCAACG 1053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
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                                                                                                              INVENTION: RAPID DETECTION AND IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 135.6; DB 11; Length 54.1%; Pred. No. 1.5e-31;
Live 0; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REDADLE PORM:
CMEDIANTREE: ROOPS disk
CMHOTTER: IBM TO COMPARIALE
OFFICERATING STEER: PC-DOS/MS-DOS
SOFTWARE: Patentin, Release 1.0. Version #1.30
                                                                                                                                                                                                                                                                                       STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGRIT INCORNATION:

NAME: ARROLL. PETER 6.

REGISTRATION NUMBER: 20, 337

REPRESCANTON INCORNATION:

TELECOMMUNICATION INCORNATION:

TELERA (415) 397 4838

INFORMATION FOR SQL ID SOL 143:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/940,925A FILING DATE: 10-Jun-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 143:
US-09-940-925A-143
                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                      LYAMICHEV, VICTOR I. OLIVE, DAVID M.
                                                                                                                                                     PATHOGENS
              APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              CITY: SAN FRANCISCO
                                                                                                                                                                                  SEQUENCES: 165
                                                                                                                                                                                                                                                                                                                                                                STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 329; Conservative
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                                                                                                                   TITLE OF
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1174 GCCAGCGACCCTCTATTCGCCACAACCCGATCATGACCGATGCGGATATGGCGATAAAG 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             994 GGCAAGGCAAGCAACGCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAACCCCACG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1114 CCTGCCGGTGCCCACCATTGGGAACCGATTGACATAAAAGGAAAACAAGCCGGTTGAC 1173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1354 TACATCGGCCCGGAAGTGCCGGCAGAAGACCTGATTTGGCAAGACCCGATTCCGGCAGGT 1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 137.2; DB 11; Length 620;
Pred. No. 4.7e-32;
0; Mismatches 263; Indels 15; Gaps
                                                                                           NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 33,337
REFERENCE/DOCKET NUMBER: 23,337
REFERENCE/DOCKET NUMBER: FORS-01756
TELECHMULICATION IRROBATION:
TELEPRAN: (415) 705-8110
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 150:
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FILING DATE: 28-Aug-2001
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.3%;
Matches 330; Conservative C
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Length 620;

1414 AACACCGACTACTGCGAAGAAGTGG------TCAAGCAGAAAATTGCACAAAGT 1461

1233

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312

1521

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1234 GTAAATCCGACCTATCGCGCTATCTGCGAAAAATTCATGGCCGATCCTGAGTACTTCAAG 1293
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                                                                                                                                                                                                                                                                                        553 AGGGACAAAGGGGGGGGGGCGCCAACGGTGGTCGCATCGCCTGCAGCCACAAGTCGGGTGG 612
          136 CCTGCTGGCGCTTGGCAATACACCCGCCAAGGACGGCGGCCGGTGCCGGCACCATCCCGGAC 195
                                                                                             196 CCGTTCGGCGGGCC---AGGGCGCTCCCCGACGATGCTGGCCACTGACCTCTCGCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                            1174 GCCAGCGACCCCTCTATTCGCCACAACCCGATCATGACGGATGCGGATATGGCGATAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1462 GGCCTGAGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCGTACTTATCGCGGT
                                                                                                                                                                                                           493 GGATTGACTGTCTCACAGCTAGTTTCGACCGCATGGGCGGCGCGCGTCGTCGTTCCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BROW, MARY ANN D.
LIAMACHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1,30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: THOPPY CARACTER COMPUTER: TEM PC compatible OPERATUR SYSTEM: PC-105/MS-105 CURRENT APPLICATION DATA: TLING TO THE CARACTER CARACTER (1099/940, 925A FILING DATE: 10-Jun-7002 CLASSIFCATION: CURKOWA: ATTORREY/AGDM THROBANTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: FORS-01756 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 147, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
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TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 147;
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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                                                                                                                                                    1522 TCCGATATGCGCGGCGGTGCTAACGGTGCCCGCATTCGCTTGGCCCCACAGAACGAGTGG 1581
                                                   1462 GGCCTGAGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCGGTACTTATCGCGGT 1521
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133 AGCCACGACCTCGTCGGCGAAGCCGAGATTGCCAGCCTTAAGAGCCAGATCCGGGCATCG 492
                                                                                                                                                                                                     553 AGGGACAAAGCGCGGCGGCGCCAACGGTGGTCGCATCCGCCTGCAGCCACAAGTCGGGTGG 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1,5e-31;
ches 264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGREY INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REPERREKE/CACET UNMBER: PORS-01756
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/940,925A
FILING DATE: 10-Jun-2002
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-09-940-925A-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 145, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
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TELEPAX: (415) 997-8338
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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994 GGCAAGGCAAGCCAACGCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAACCCCACG 1053
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Pred. No. 1.5e-31;
0; Mismatches 264; Indels
                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUTCATION INFORMATION:
TELEPAN: (415) 705-8410
TELEPAN: (415) 397-8338
INFORMATION FOR SEQ IN NO: 149;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                APPLICATION NUMBER: US/09/940,925A FILING DATE: 10-Jun-2002 CLASSIFICATION: <UNKNOWN>
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SEQUENCE DESCRIPTION: SEQ ID NO: 149:
US-09-940-925A-149
                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.0%;
Best Local Similarity 54.1%;
Matches 329; Conservative
   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AGCCACGACCTCGTCGCGAAGCCGAGATTGCCAGCCTTAAGAGCCAGATCCGGGCATCG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 GGATTGACTGTCTCACAGCTAGTTTCGACCGCATGGCCGCCGCCGTCGTTCCGTGGT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 cerecresedentedecantacaceccaaceacecceseccesedecarecesace
                                                                                                                                                                                                                                                                    994 GGCAAGGCAAGCAACGCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAACCCCACG
                                                                                                                                                                                                                                                                                                      545 AAATGGGACAACAGTTTCCTCGAGATCCTGTACGCTACGAGTGGGAGCTGACGAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 CCGTTCGGCGGGCC---AGGCGCTCCCCGACGATGCTGGCCACTGACCTCTCGCTGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 AGCGACAAGCGCGGCGCGCAAACGGTGGATCCGCCTGCAGCACAAGTCGGGTGG
                                                                                                                                                                                                                    Gaps
                                                                                                                                                            DB 11; Length 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                0; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAW FRANCISCO
STATE: CALIFORNIA
COUNTRY: 101TED STATES OF AMERICA
                                                                                                                                                            Score 135.6; DB 1
Pred, No. 1.5e-31;
                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 147:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 149, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYAMICHEV, VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHOGENS
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STRANDEDNESS: double
                                                                                                                                                            6.0%;
54.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 165
                                                                                                                                                                                  Best Local Similarity 54.19
Matches 329; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1582 CAGGGCAA 1589
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US-09-940-925A-147
                                                                                                                                                            Query Match
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5         246.2         10.9         742         13         BO751812         BO751808         BO751801         BO751801         BO751807         BO751807	ALIGNMENTS  AREQUIT 1  AREO7865  LOCUE  ACCESSION  ACO7865  ACO7865  ACO7865  ACCESSION  ACO7865  ACCESSION  ACO7865  ACCESSION  ACO7865  ACCESSION  ACO7865  ACCESSION  ACO7865  ACCESSION  ACO78665  ACCESSION  ACO7866  ACCESSION  ACCE
GenCore version 5.1.6  Copyright (c) 1993 - 2003 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: October 8, 2003, 07:49:13; Search time 4688.37 Seconds (Arthout alignments)  1726.187 Million cell updates/sec  Title: GS-09-884-889-5  Sequence: 1 atgataacgcatccgctgagtttcgacgtcgctgcgtca 2262  Searched: 22781392 seqs, 12152238056 residues  Total number of hits satisfying chosen parameters: 45562784  Minimum DB seq length: 0 GS-09-884-889-5  Maximum Match 1008  Listing first 45 summaries  Database: EST:*  1	to the score of the result being printed, of the cotal score distribution.  SUMMARIES  ID  Description  AR075865  AR075865  AR075861  BG75115  BG751112  BG751112  BG751112  BG370112  BG370112  BG370112  BG370112  BG370112

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                                                                                                                               2171 CCCAGGACGATAACG-GCGAGAAGTTCGTCGAGACTTCGTCGCCGCCTGGACGAAAGTG 2229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Deborah A. Samac
Department of Parison Pathology
University of Minnesota
101/secilor of Minnesota
195 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
1945 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
1955 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
1955 Borlaugh 1955 Borlau
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/mo.Lype=mRNA*

/mo.Lype=hRNA*

/db.xef=taxon:546*

/clone='poscyr'68*

/fisheu_type="wrocile"

/dev_stage='voung_actively growing mycelia (3 days after
inoculation) grown in liquid culture (cutin minimal medium
containing 28glucose).

/ab_host="pisalpha"
                             150 CGGTACTICCAACAAAATIGGIGGCCGGAAGGGTIGAACCTGGATAITITGCAICAGCA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes; Sordariomycetes incertes sedis; Phyllachorates, Phyllachoraces, mitosporic Phyllachoraces; Collectrichum.

1 (bases it CD 707)
Samac, D. A. Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
ESTS from mycella of Colletotrichum trifolli race I uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2.4e-60;
0; Mismatches 166; Indels 0;
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Location/Qualifiers
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Colletotrichum trifolii
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Best Local Similarity 68.5%;
Matches 361; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            732 TCAGCACTGACTTCTTCGCTAATCTGCTGGATATGCGTTACGAGTGGAAGCCCACCGACG 791
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Amoutype="gamonelle typhimurium"

Moutype="gamonel DNA"

Motor="172"

Motor="172"

Motor="172"

Motor="173"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1347 ATCACGTTACATCGCCCGGAAGTGCCGGCAGAAGACCTGATTTGGCAAGACCCGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 CGGCGGCGATAAGCGTGGCGCGCTAACGGCGCGCGTCTGGCATTAGCGCCTCAGCGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1287 CTTCAAGAAACTTTCGCGAAGGCGTGGTTCAAGCTGACGCACGGTGACCTGGGCCCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 CTTTAATGAAGCCTTTGCTCGTGCCTGGTTCAAACTGACGCACAGAGATATGGGACCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 GCAACCGCTCTATCAGCCAACGCAGGAAGACATTATCAACCTGAAAGCGGCGATCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGTGGCCTGAGCATTAGTGAGATGGTCTCCACCGCTTGGGACAGTGCCCGGTACTTATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 ATCCGGGCTTTCTATTAGCGAGATGGTTTCGGTTGCCTGGGCATCCGCGTCTACTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1637 CTGCCGACACCGGCGCTAGCATCGCGGACGTGATCGTTCTGGCCGGTAGCGTAGGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 285.2; DB 28; Length 159.9%; Pred. No. 8.7e-67;
tive 0; Mismatches 372; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 t
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a 278 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 59.9
Matches 587; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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0   0   0   0   0   0   0   0   0   0	QY 450 GCTCAACTCCTGGCCGGACAACGTCAGCTGGATAAAGCGCGCGTGTGGCCGTT 509	OY 510 CAAGAAGAAGTACGGCAACAAAATCACCTGGGCAGACGTATGATGATGTGGGTGG	0y 570 decreaserchaserchaserchaserchaserchaser (629 11   1   1   1   1   1   1   1   1   1	QY 630 GGAACCCGAAAAAAAAAAAATCGGGGGGGGGGGGGGGGG	RESULT 3 BQ752115 BQ752115 COUGUS ESR623678 DSCT COlletotrichum Trifoll1 CDNA Clone pDSC710-12, mRNA ACCESSION BQ752115 BQ752115 GG1600000000000000000000000000000000000

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Other ESTS: EST632443
Contact: Deborath A. Samac
Contact: Deborath A. Samac
Department of Plant Pathology
University of Minnesota
403 Borlang Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Fax: 61 625 5038
Fax: 61 649 5038
Fax: 61 649 5038
TIGR Sequence name: WTSA12TV Wore Information is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 CGGCATCAAGAACCGCGACTGGTGGCCGGATGCGCTGAAGCTCAACATCCTCCGCCAGCA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 AGATCGCAAATCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 CGATTTCGACGCGCTGAAGAAGATGTCCACGCGTTGATGACCGATAGCCAAGAGTGGTG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 cGACTACGAGGGGGTCAAGAAGGACCTCACGGCCCTGATGACCGACTCCCAGGACTGGTG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 GCCCGCTGACTGGGGGCACTACGCCGGTTTGATGATCCGTATGGCTTGGCACTCCGCTGG 389
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                 EST632444 DSCT Colletotrichum trifolii cDNA clone pDSCT8-27, mRNA
                                                                                                                                                                                                                                                                                                         Enkaryota: Pund; Ascomyocta: Pezizomyoctan; Sordariomyeetes; Sordariomyeetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; collectrichum.

1 (bases i Co 742)

5 mato. Ja., Jackman, M., Town, C.D., Van Akan, S., Utterback, T., Samach, D.A., Jackman, M., Town, C.D., Van Akan, S., Utterback, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 CACGCCCGTCACCAACCCGCTGGGCCAGGACTTTGACTACGTCGCCGCCTTCAAGTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheung, F. and Fraser, C.M. ESTs from mycella of Colletotrichum trifolii race 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.6e-56;
0; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Colletotrichum trifolii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: (9th AtA CgA CtC ACt AtA 999 C).
Location/Qualiflers
1, ,742
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/strain="race 1"
/db_xref="taxon:5466"
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                                                                                                                                                                                                                           Colletotrichum trifolii
Colletotrichum trifolii
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Best Local Similarity 67.9%;
Matches 359; Conservative
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                                                                                                     BQ751881
BQ751881.1
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                 DEFINITION
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ORIGIN
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 GGTGGTTTCTTCATCCGATTGGCATGGCACGCCCGGTACCTATCGTGTCACGGATGGC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 TGGCCAAACGAGCTGAGGACCAACATCCTCGGCAGGACGATCCCCGCCAAAACCCTCTC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGGGGGGGGGGTACCGGAAGCCAGCGCTTTGCACCGCTCAACTCCTGGCCGGACAAC 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 GATGTCCACGCGTTGATGACCGATAGCCAAGAGTGGTGGCCCCCCTGACTGGGGGGCACTAC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGGTTTGATGATCCGTATGGCTTGGCACTCCGCTGGCACCTACCGTATTGCTGATGGC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 CGTGGTGGAGGTGGCGAAGGACAACAGCGCTTTGCCCCTCTCAACTCATGGCCCCGACAAT 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   532 ATCAGCTGGGCAGACCTGATGTTCTGGCTGGCACCGTGGGCTTATGAGTCCATGGGCTTA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 CCTGCTTACGCCTTCTCTTTCGGCCGCGTCGATATTTGGGAACCCGAAAAAAATTTTTAC 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 TGGCCGGAAGGGTTGAACCTGGATATTTTGCATCAGCAAGATCGCAAATCAGACCCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                            Contact: Alexander Idnurm
Barbara J. Howlett (bhowlettéunimelb.edu.au)
School of Bocany
The University of Melbourne, Parkville, VIC, 3010, Australia
The University of Melbourne, Parkville, VIC, 3010, Australia
The 15 13 8134 5056
Fax: 61 3 9147 506
Fax: 61 3 9147 506
Seq primer: 31 Universial Primer.
Location/Qualifies
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/db_rref-taxon:5022*
/dclone_iib=108 mycelial library*
/dote-library prepared from mycelium grown in 108
/mote-library prepar
           ŏ
Expressed sequence tags of Leptosphaeria maculans, cause blackleg disease of oilseed Brassicas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 257.8; DB 10; Length
Pred. No. 2.1e-59;
0; Mismatches 187; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, .562
/organism="Leptosphaeria maculans"
/mol.type="mnna"
/strain="Mn"
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546 TGGGAGGCGAGACAGA 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.41
Matches 370; Conservative
                                                                                   Unpublished
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BQ751881
LOCUS
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     TITLE
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BASE COUNT 131 a 222 c 176 g 110 t	Query Match 10.4%; Score 236; DB 13; Length 639; Best Local Similarity 68.3%; Pred. No. 2.1e-53; Matches 326; Conservative 0; Mismatches 150; Indels 0; Gaps 0;	dy 150 cogracticcaacaadariogrocogaaagogigaacciogaratifocarcagca 209  16 cogracticcaacaacgccaargogocogariocorcaacrccaacarcercaccaccaca 223	dy 210 AGATCGCAAATCAGCGATGGATCGGGATTTCAACTACCGTGAAGAGGT 269 224 CAGCCGGTCACAACCGCTGGGCAAGATTTGATTGATGGTCGCCGCTTGAAGTCGT 283	dy 270 CGATTTCGACGCGCTGAAGAAAGATGTCCACGCGTGATGACGGATAGCCAAGGGGGG 339  Db 284 CGACTACGACGCGCTCAAAAGAACGACCTCCATGACGACTGCAACTCCCAGACTGCACTGCTGAAAGAACGACCTCAAAAGAACGACCTCAAAAGAACGACCTCAAAAGAACGACCTCAAAAGAACGACCTCAAAAGAAAG	Qy   330 GCCCGCTGACTGGGGCCACTACGCCGTTTGATCATCCGTATGGCTTGGCACTCCCGTGG 389		QY 570 GGCTTATGAGTCGATGGGCTTACCTGCTTACGGCTCGGCTCGGTGGATA 625	RESULT 7 BQ751307 LCCUS BQ751387 CCUS BQ751387 DEFINITION EST631950 DSCT Colletotrichum trifolli cDNA clone pDSC74-87, mRNA	ACCESSION SEQUENCE.  VERSION BQ751387.1 GI:21906792  KEYWORDS EST. SUGMECTICHMA ITIEQIII ORGANISK COllectichma trifolii			Depot Lamet, of Aranic Farancia of St. Paul, MN 55108, USA 495 Borlang Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA Tel: 612 625 143	EMAIL: debDy8@gecoin.cit.umn.edu TIGR sequence name: MTSAB9TR More information is available at: www.medicago.org Seq primer: SRmod (CTA gAA CTA gtg gAT CC). FEATURES 1. cOctlon/Qualifiers Source 7. coctlon/Qualifiers 1. coctlon/Qualifiers	/ordantsm=_correctionm_critotii_
Oy 390 CACCTACCGTATGCTGATGGCGTGGGGGGGTGGTACCGGAAGCCAGCGCTTTGCA 447	OY 448 CCGCTCAACTCCTGGCGGACAACGTCAGCCTGGTATAAACGCGCGCTCTGCTGTGCGCG 507	OY 508 PACAGAAGARCACCACAACAAAATCAGCTGGGCAGACCTGATGATTCTGGCTGG	Oy 568 GIGGCTARIGAGICCARGGCTTACCGCCTTCTTCGGCCGCGTCGATAT 627  Db 580 GIGGCTCCACATCCATGCGTTTCACGGCGGCTTCTCGCCGACGCGTCGATAT 627	9y 628 TGGGAACCCGAAAAAGATATCTACTGGGTGGGAAAAAGAGTGGCTGG 676  Db 640 TGGGAAGCGAAGAACACGTCGGTTACTGGGAAAAAACCACGGGGGGGG	RESULT 6 80751312 LACUS B0751512 679 bp mRNA linear EST 18-JUL-2002 DEFINITION EST632075 DECT ColletoLichum trifolli cDNA clone pDSCT5-66, mRNA	ACCESSION sequence. VERSION BO75111.1 G1:21906917 VERYWORDS EST. SOURCE COllectrichum trifolii ORGANTS COLLECTRICHUM trifolii	AUTHURS SEMECTIA. LUCKMEN, TOWN.C.D., Van Aken,S., Utterback,T., TITLE EST9 from mycella of Colletotrichum trifolli race 1 JOURNAL Unpublished COMMENT Other EST9: EST612074	Contact: Department of Flant Pathology University of Minnesota 495 Borlang fall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA Tel: 612 655 1243	Enail: Gebbys@toctof.orl.umn.edu Trick sequence name: MTSRE6GTV More information is available at: www.medlcago.org Seq primer: (gtA ARA CgA CCC ACC ARA ggg C). FRATURES Location/Oualifiers	rce	/dazte=-taxon:seto- /clone=-pgcf=-66* /tissue_type=-mycelia* /tissue_type=-young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing ?Aglucose).	/clome_libe_bSCT* //clome_libe_bSCT* //clome_vector: pBluescript SR+; Site_1: EcoRI; Site_2: EcoRI; isolate: Sap2 : clNA was prepared from polyA+ enriched RNA The clNA was ligated into Lambda gill from	Stratugeme and packaged using Gigapack packaging extracts.  An aliquot of the amplified library was used to transduce E. coli X1090 and phage Dwit May was purified from a liquid lysate. The CDMA inserts were gel purified after EcoRI digestion and ligated into palwescript SR. Aliquots of the ligation were used to transform E. coli Disfalpha which were plated onto medium with X-qal for selection of	אפרה הימינה סוורת והפתיחהה אדרה ים אמד דמן מפדפנורים מי

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151 GGTACTTCCAACAAGATTGGTGGCCGGAAGGGTTGAACCTGGATATTTTGCATCAGCAA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pSPORTI; Library constructed from cultures utilizing ammomium ions as a source of nitrogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 GATCGCAAATCAGACCCGGATGCGGATTTCAACTACCGTGAAGAAGTACGCAAGCTC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 GGTACCCGCAACAGGGACTGGTGGCCAAATGAGCTGAACACCAAGATCCTGCGCCAGCAC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 ACCGCTGCTACCGACCCATTCGGCAAGCAGTTCGACTACCCAGCCGCATTCAAGAGCTTG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 GATTTCGACGCGCTGAAGAAGATGTCCACGCGTTGATGACCGATAGCCAAGAGTGGTGG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCGCTGACTGGGGGCACTACGGCGGTTTGATGATCCGTATGGCTTGGCACTCCGCTGGC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCTACCGTATTGCTGATGGCCGTGGGGGGGGGTGCTACCGGAAGCCAGCGCTTTGCACCG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAACTCCTGGCCGGACAACGTCAGCCTGGATAAAGCGCGCCGTCTGCTGGCCGATC 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAACTCATGGCCGGACAACGCCAATCTCGACAAGGCTCGCCGCTGTTGTGGCCAATC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCAAAAGTACGGAAACAAGATCTCATGGGCCGACCTGTTCCTCCTCACTGGAAATGTC 511
                                                                                          1 (bases 1 to 729)

Koon, Jr. B., Balley A.M. and Hargreaves, J.A.

Koon, Jr. B., Balley A.M. sequences from the wheat fungal leaf
blotch pathogen, Mycosphaerella graminicola (Septoria tritici)

2014012 Genet. Biol. 29 (2), 118-133 (2000)
                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 233.2; DB 9; Length Pred. No. 1.3e-52; O: Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Mycosphaerella graminicola"
                                                                                                                                                                                                                                                                                                                                                                             Email: john.hargreaves@bbsrc.ac.uk
Insert Length: 2600 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 t
                                                                                                                                                                                                                                                  Contact: Hargreaves JA
Contact: Hargrey Department
IACR-Long Ashton Research Station
Cong Ashton Bristol, BS41 9AF, UK
Tel: +44(0)1275 332181
Fax: +44(0)1275 332181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:54734"
/clone="MgA0020"
/clone_lib="MgA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 reverse.
Location/Qualifiers
Mycosphaerella graminicola
Mycosphaerella graminicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type-"mRNA"
/strain-"Strit"
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343; Conservative
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                                                                                                                                                                                                    Anote-Vector; philuserity SK+; sited:: EcoRi; sited::
ECORI; isolate: Jap2; cDNA was prepared from polyA-from
enribhed RNA The cDNA was ligated into Lambda gill from
Stratagene of apextoged using Gigaper perkapting extracts.
An aliquoof the amplified library was used to transduce
E. COLI INO9 and phage DNA was purified from a liquid
Ilyante. The CDNA inserts were gel purified after ECORI
disperion and liquoted into philoserity SK+ aliquots of
the liquion were used to transform E. COLI DRSIAND were plated onco medium with N-gal for selection of
                                                    /closee.ppscr4.87*
/fissue_type="wordle".
/dev_stage="foung, actively growing mycella (3 days after-fincellation) grown in liquid culture (cutin minimal medium containing 74glucose).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 CGGTACTTCCAACAAGATTGGTGGCCGGAAGGGTTGAACCTGGATATTTTGCATCAGCA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCATCAAGAACCGCGACTGGTGGCCGGATGCGCTGAAGCTCAACATCCTCCGCCAGCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 AGATCGCAAATCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 CGACTACGAGGGCGTCAAGAAGGACCTCACGGCCCTGATGACCGACTCCCAGGACTGGTG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWI79968
M9A0300 MGA Library Mycospherella graminicola cDNA clone M9A0020
5 Similar to catalase-peroxidase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGATTICGACGCGCTGAAGAAGATGTCCACGCGTTGATGACCGATAGCCAAGAGTGGTG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCGCTGACTGGGGGCACTACGCCGGTTTGATGATCCGTATGGCTTGGCACTCCGCTGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCTACCGTATTGCTGATGGCCGTGG-GGGCGGTGGTACCGGAAGCCAGCGCTTTGCAC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569 TGGCTTATGAGTCCATGGGCTTACCTGCTTACGGCTTCTCTTTCGGCCGCGTCGATALTT 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 CACGCCCGTCACCAACCCGCTGGGCCAGGACTTTGACTACGTCGCCGCCTTCAAGTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 234.8; DB 13; Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.4e-53;
0; Mismatches 152; Indels
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                                   /db_xref-"taxon:5466"
                                                                                                                                                                                                                                                                                                                                                                                                                                     172 g
                                                                                                                                                                                  /clone_lib-"DSCT
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68.8%;
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                              214 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.4
Best Local Similarity 68.8
Matches 337; Conservative
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us-09-884-889-5.rst

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Chromatogram file of this sequence is available, see contact person isset in tht (April. 22, 2003) 9blAnk65352, catalase-peroxidase (Neurospora crassa) >91126921. . . 288 4e-77
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/sar-"hat1.2 hermaphrodite"
/cell_type-"Appressorlum'
/clone_lib-"haraporthe gisea Ap Uni-Zap XR Library"
/clone_lib-"haraporthe gisea Ap Uni-Zap XR Library
/clone_library
/clone_library
/clone_library
/cell_type-"haraporthe gisea Ap Uni-Zap XR Library
/cell_type-"haraporthe gisea Ap Uni-Zap XR Library
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/clone
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MBNA linear EST 06-MAY-2003

MGP008xD18f.b Magnaporthe grisea Ap Uni-Zap XR Library Magnaporthe
grisea const clone mgap008xD18 5', mRNA sequence.

MGE5076

BMS6076

BMS6076

BMS6076

MGR ST 01:30390127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1051 ACGAAATTCGATATGGGCTATTTCGACCTGCTGTTCGGCTACAATTGGGAACTGAAAAAG 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       992 AGGGCAAGGCAAGCAACGCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAACCCC- 1050
                                                                                                                                                                                                     931
                                                                                                  112 AGC-GATTCGTGCGACCTTCGGCAACATGGGCATGAAGAAGAGACGTCGCGCTGA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651 ACCCAGTGGAGCAACTACTTCGAGAACCTGTTCAAATACGAATGGGTACAGACCGC 710
353 GCCTGATCTACGTGAACCCGGAAGGCC-GAACGCCAGCGGTGAACCGCTGTCAGCGCGGC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Megnaporthe grisse (anamorph: Pyricularia grisse)
Megnaporthe grisse
Megnaporthe grisse
Medrayota: Paricumycotina: Sordariomycetes;
Sordariomycotes Incertae sedis; Megnaporthaceae; Megnaporthe.
Bloboses 1 to 66:1)
Elbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatterai.
K. and pean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                      872 CAGCTGGCGGCCACACCGTCGGTAATTGTCACGGTAATGGCAATGCCTCTGCGTTAGCCC
                                                                                                                                                                                                                                                                                                                                         932 CTGACCCAAAAGCCTCTGACGTTGAAAACCAGGGCTTAGGTTGGGGCAACCCCCAACATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591 CGCCGGTTGCCCCTGATGCCCATTACCTCCGGTCTGGACAGTCATCTGGTCAAACCCCG
                                                             812 AGCAGGTACTTGAAACCTTCGCCCGTATGGCGATGAACGACGAAAAAACCGCAGCCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002 this sequence version replaced gi:19232758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on Mar 7, 2002 this sequence version replaced g1:19232779 confact: EBDALB DV borned: EBDALB DV benthered of Plant Pathology & Wicrobiology Peterson Bidg, M83132, College Station, TX 77843-2132, 13.5 mis 1979 645 4031 Fear: 979 845 4031 Email: d-obbole@tamu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Magnaporthe grisea"/mol_type="mRNA"
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/db_xref-"taxon:148305"
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Plate: mgap008 row: D column:
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BACKWARD: T7 primer
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                                                                                                                              GSS 01-JUN-2001
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                                                                                                                     CMSOlHHH

CARDpletes gambiae GSS SP6 end of Clone OBMOS of Notrabanal library

Arom strain PEGF of Anophales gambiae (African malaxia modulto).
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Submitted (16-28B-2000) BBMI, Institut Pasteur, 25, rue du Dr. Beux, Perris 75015, France Roux, Perris 75015, France This cione is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in Collaboration with the Location and Sequence of Genoscope in Collaboration with the Location and BAC library of Bacchem. and BAC. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Poptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Anopheles gambiae
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Pred. No. 3e-50;
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/clone="08M05'
/clone_llb="NotreDame1"
/note="end : SP6'
a 217 c 224 g 127
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/mol_type="genomic DNA"
/strain="PEST"
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Best Local Similarity 60.6%;
Matches 453; Conservative
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VERSION
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                                                        RESULT 9
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Paul, MN 55108,

is available at:

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//note=Vector: pBluescript SK+: Site_1: EcoRI; Site_2:
EcoRI; isolate: 1282; colonk was prepared from polyAr
EcoRI; isolate: 1282; colonk was prepared from polyAr
Statagene and peckaged using Gigaptor packaging attracts.
An aliquot of the amplified library was used to transduce
E. coli 1109 on and phage now was purified from a liquid of
Hyaste. The CDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+: Aliquots of
the ligation were used to transform E. coll BMRalpha which
were plated onto medium with X-9al for selection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /fissuc_type="yepla"
//dev_stage=type=type=type
//dev_stage='Young actively growing mycelia (3 days after
//dev_stage='Young actively growing mycelia (outin minimal medium
containing %galosee.'
//dab_hosic_eighad.
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Pred. No. 2.3e-48;
0; Mismatches 224; Indels
         ESTS from mycelia of Colletotrichum trifolii race Unpublished
                                                                               Ochici_BSTW: BSS%430678
COUTLOG' DODOTCH, A. Sumer
Department of Minnesota
Miversity of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Colletotrichum trifoli1"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
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predominantly 5' reads. T7 primer on XhoI side of insert. Appressorium inforary. Condia were garm inated on an inductive surface for 5-8 h. Sequences were processed by one of two methods. Where a full-inquth alignment to the M. grisse genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredphrap variation 991019 and trimmed according to phd files (0.05) and for vector
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1 (bases 1 to 633) to 630, 100 to 600, 100 to 600 t
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6; Gaps

Length 633;

1767

1827

443

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323

Duery Match  9.6%; Score 217; DB 14; Length 757; Best Local Similarity 63.9%; Pred. No. 3.6e-48; Matches 328; Conservative 0; Mismatches 155; Indels 0; Gaps 150 Conservative 0; Mismatches 150 Conservative 150 C	Db 216 TICGCCTCAGTATAACCCATTGGGTGCTGATTGACTACACGAGGCTTTCAAGTCTC* 275  270 CGATTCCAACGCGCTGAAGAAGATGTCCAACGCGTTGATGACCAAGAGTGGTG 329  270 CGATTCGACGCGTGAAGAAGATGTCCAACGCGTTGATGAAGAGTGGTG 339  276 GGACTTTGCTGCATTGAAGAAGACCTCAACGGGCTTCACATGATGATGGTG 339  Qy 330 GCCGCTGACTGACTGGGGGGATTGAAGAGGGGTTTGATGGTG 389  Db 336 GCCGCTGAACAGGGGGAAATTGAAGATGGTGGTGGTGGTGGTGGTGGTGG	390 CACCTACCGTATGCTGATGGCCGTGGGGGGGTGTATCCGAAGCCAAGCGCTTTGCACC	0   0   0   0   0   0   0   0   0   0	RESULT 13 AW180683 AW180683 TO THE STATE OF	DOURNAL Pungal Genet. Mycosplacrella graminicola (Septoria tritici) MEDICE 20174020 EN 29 (2), 118-133 (2000) MEDICE 20174020 EN 2017
	۸ خ	VERSION CD423096.1 G1:31331359 VERSION CD423096.1 G1:31331359 VERSION CD423096.1 G1:31331359 SOURCE SOTOMUM Dicolor (Sorghum) ORGANISM ENATYOLE: VILIGIPABRIES STEPPOPOPHYES; Embryophytes; Fracheophytes; Spermatcophytes; Miniophytes, Liliopsida; Poales; Poaceae; PACCAD REFERENCE 1 (Dass 1 Lo C):		International Control of the Control of Co	//Longe-Sall-Quela, Duck John Long And John Long Library Ball Cyling and Table Long Library Ball Cyling and Table Ball Cyling and Table Ball Cyling and Table Ball Cyling and Table Ball Cyling Library Ball BB-Fil; Site 1: Xhoi; Site 2: Xhoi; The Interary was prepared from polyak Run from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 1 mM sallcylic acid (SA). Roots and shoots were harvested affer 27 and material from bouble-stranded CNN was combined prior to RNA isolation. Double-stranded CNN was cioned undirectionally into different Daili sites of the pRENBS-Fil vector (5-prime Draili site La CACCANGTG).  1.Xhoi excises the CDNA insert.

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Ablance—taxon 4558.

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(Lone—153, 13 HILD A002-resistant E. coll*

(Ablance—bette billor—il phage-resistant E. coll*

(Ablance—Vector: philos—il phage-resistant E. coll*

(Ablance—Vector: philos—il site_i: Ahoi; Elee_i: Xhoi; The

(Ablance—Vector: philos—il site_i: Ahoi; Che seedlings grown

In Marcoponto culture. At 8 days of age, medium was

supplemented with im Salicyll codd (Sa). Rocors and

shocks were harvested after 27 and 72 hr and material

boots were points was combined profit or RA Isolation.
                                                                                                                                                                                              Library Constructed by Dr. Yutaka Sizuki, and Dr. Sumio Sugano in the Human decome center, University of Tokyo Institute of Medical Science plant material and RNA prepared at Texas a s W University, Sequencing done in the Laboratory for denomines and Bioinformatics, University of Georgia. Sequence ends have been trimmed to acclude are presented as their reverse complement and have been trimmed to
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Contact: Confoming-Prett MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Deportment of Plant Biology
Than Sciences Building, Em. 2502, Athens, GA 30602-7211, USA
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63.1%; Pred. No. 2.5e-45;
11ve 0; Mismatches 185; Indels
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="BTx623"
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                                                                                                                                                                           Email: mmpratt@uga.edu
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317; Conservative
                                                                                                                          Tel: 706 542 1860
Fax: 706 583 0210
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1..573
/ Organisa-Wycosphaerella graminicola-
/ Organis-Wycosphaerella graminicola-
/ Mol. Lype-mRNA
/ Gland-Strift
/ Clone-Wycospis-WyA Library
/ Clone-Wycotor: pSPORTI; Library constructed from cultures
utilizing ammendum long as source of nitrogen
a 171 c 147 g 122 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                151 GGTACTTCCAACAAGATTGGTGGCCGGAAGGGTTGAACCTGGATATTTTGCATCAGCAA 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 ACCGCTGCTACCGACCCATTCGGCAAGCAGTTCGACTACCCAGCCGCATTCAAAAGCTTG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 GATTTCGACGCGCTGAAGAAGATGTCCACGCGTTGATGACCGATAGCCAAGAGTGGTGG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCTACCGTATTGCTGATGGCCGTGGGGGGGGGTGGTACCGGAAGCCAGCGCTTTGCACCG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        571 GCTTANGAGTCCANGGGCTTACCTGCTTACGGCTTCTTTCGGCCGCGGTCGATATTTGG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorghum bicolor
Enkaryota, Yirldiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnollophyta; Lillopaida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disses 1 to 701)

Cordonier-Pritt, M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R., Chun, R. W., Gorzalez, M., Lane, S., Miller, V., Nanda, P., Olaseinde, O., Estiman, A. and Frett, L.H.
An Estiman, A. and Frett, L.H.
An EST database from Sorghum: salicylic acid-treated seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 GATCGCAAATCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                         Length 573;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                      Score 208.4; DB 9;
Pred. No. 7.3e-46;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorghum bicolor (sorghum)
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                                                                                                                                                                                                                                                                                      9.2%;
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I (Dasal 10 712)
Trail,F., Xu, Y.-F., San Miguel,P., Halgren,R.G. and Kistler,H.C.
Analysis of expressed sequence tags from Gibberella zeae (anamorph Fungal Genet. Biol. 38 (2), 187-197 (2003)
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//db_xref="taxon=5518"
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Pred. No. 5.2e-44;
0; Mismatches 233; Indels 3;
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                                                               630 GGAACCCGAAAAAGATATCTAC 651
                                                                                                           680 NGAAGCCGATGAGTCCGTCTAC 701
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Search completed: October 8, 2003, 15:29:18 Job time: 4695.37 secs THIS PAGE BLANK (USPTO)

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 19:31:22; Search time 60.8231 Seconds (without alignments) 1965.061 Million cell updates/sec October Run on:

US-09-884-889-6 4058 Perfect score:

1 MNNASADDLHSSLQQRCRAF......RDFVAAWTKVMNADRFDVAS 753 BLOSUM62 Scoring table: Sequence:

1107863 seqs, 158726573 residues Gapop 10.0 , Gapext 0.5 Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_19Jun03:\* Database

2 (2012) (1999a to 2) (1990a to /SIDS1/gcgdata/geneseg/genesegp-embl/AA1980.DAT:\* /SIDS1/gcgdata/geneseg/genesegp-embl/AA1981.DAT:\*

Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

## SUMMARIES

Description	Alcalidenes (Delev	Alcalidenes catala	Amino acid sequenc	Microscilla furves	Mycobacterium tube	M. tuberculosis ca	Mycobacterium tube	M. tuberculosis ca	M.tuberculosis H37
QI CI	AAW33809	ABG33040	ABB78212	AAW33810	AAW26596	AAW95398	AAW31343	AAW95399	AAR43670
BB	19	23	23	19	18	50	19	50	14
% Query Match Length DB	753	753	723	745	740	740	740	740	735
% Query Match	100.0	100.0	69.5	56.4	50.4	50.4	50.3	50.3	46.6
Score	4058	4058	2820	2290.5	2044.5	2044.5	2041.5	2041.5	1890
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735	731	533	2	1550	201	291	246	354	426	426	452	250	250	250	250	250	250	250	250	254	297	297	215	215	215	215	215	215	215	347	348	353	353	279	348
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## ALIGNMENTS

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Catalase; epoxidation; hydroxylation; biosensor; paper bleaching;
                                                                                                                                                                             Alcaligenes (Deleya) aquamarinus catalase-64CA2.
                                           AAW33809 standard; Protein; 753 AA.
                                                                                                                                  18-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                          Alcaligenes aquamarinus.
                                                                                                                                                                                                                                                  pasteurisation.
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                                                                                      AAW33809;
RESULT 1
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97WO-US16513 96US-0674887 03-JUL-1997; 03-JUL-1996;

Sanyal I; (RECO-) RECOMBINANT BIOCATALYSIS INC. Adhikary RS, Robertson DE,

WPI; 1998-086953/08. N-PSDB; AAV06554. New bacterial catalases, related nucleic acid vectors and transformed cells - used as oxidising agents and for detecting or

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Gene; ss; marine bacteria; catalase; hydrogen peroxide; enzyme.
                                                                                               Alcaligenes catalase protein 64CA2.
                        ABG33040 standard; Protein; 753
                                                                                                                                                                                                                  19-JUN-2001; 2001US-0884889
                                                                        (first entry)
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                                                                                                                                             Alcaligenes aquamarinus.
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                                                                                                                                                                                                                                                                                                                                                                                                          of hydrogen peroxide,
antibodies which bind
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N-PSDB; ABS53944.
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                                                                                                                                                                                                                                                                                                   SANYAL
                                                                                                                                                                                                                                        03-JUL-1996;
16-OCT-1997;
05-OCT-1999;
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                                                                                                                                                                                                                                                                                                 61 GLALDILEQQDRKSDPMDPDFNYREEVRKLDFDALKKDVAALMTDSQEWWPADWGHYGGL 120
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                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                   The present sequence is of the Alcaligeness aquamarinus catalase-64CA2. Cetalase-64CA2 assistance is of the Alcaligeness ordation reactions such as epoxilated may be added to detect or destroyed and the approximation. The enzyme can also be used to detect or expecting hydrogen peroxide, e.g. in commention with glyoxylia acid productory hydrogen peroxide, e.g. in commention with glyoxylia acid productory hydrogen peroxide, e.g. in commention with glyoxylia acid measurements. The acid acid of the great products and the detection and catalase-64CA2 can be used to acceed libraries for detection and purification of calls containing the enzyme. Fragments of the gene modding Catalase-64CA2 can be used to identify related sequences.
                                                                                                                                                                                                                                                                                                                                                 MNNASADDLHSSLQQRCRAFVPLVSPRHRAIRERAMSGKCPVMHGGNTSTGTSNKDWWPE
                                                                                                                                                                                                                                                                                                                                                                                  ADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPET
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destroying hydrogen peroxide, e.g. in biosensors
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100.0%; Pred. No. 0;
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This invention relates to the DNA and protein sequences of a novel to trible control of the invention of its invention or attained to catalase polygeptide. The protein of the invention of lydrogen perceits puritied catalase polygeptide. The protein of hydrogen perceits of the protein sequence of the invention is useful for modifying amail molecules. The protein of the invention is analy molecules, by mixing the protein of the fragments with a small molecule or produce a modified small molecule. The protein of the invention is also useful for catalysing biochemical reactions, for hydrolysing specifically to the protein. The nuclect acid sequences of the specifically to the protein. The nuclect acid sequences of the specifically to the protein. The nuclect acid sequences of the section is useful as a probe to determine whether a biological sample, such as a soil sample, contains an organism having the nuclect acid or such as a soil semble, contains an organism having the nuclect acids or such as a soil semble, contains an organism having the nuclect acids. As antibody that binds the cellulase procedures to isolate or purity the protein of from detection of protein of protein of the invention is useful in immunosificinty contains expanse to table, is heat resistent, and is able to the invention section is the response to repression in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purified catalase polypeptide useful for catalyzing the breakdown approper peroxide, for medifying small molecules, and for generating blodies which bind to the polypeptide
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                                                                                                                                                                                                                                                                                                                                                                    Adhikari R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 22; Fig 5; 44pp; English.
96US-0674887.
97US-0951844.
99US-0412347.
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(REAL). Rath has a promoter which is induced by a reactive oxygen species (RAT). Rath has a promoter which is induced by a reactive oxygen species (RAT) in the RAT gene can be used in the method of the invention. The specification describes a method conspication that ability of a compound to remove a ROS. The method conjust see previous that is a RATH while a RATH while is a RATH while a RATH while is a RATH while a R
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                                                   Determining the ability of a compound to remove a reactive oxygen species (ROS), useful in pharmaceutical and nutraceutical fields and search accurately fields and antioxidants, comprises providing a coil having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWQKKEYVVKPEEMLLDRAQLMGLTGPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 SGKCPVMHGGNTSTGTSNKDWWPEGLNLDILHQODRKSDPMDPDFNYREEVRKLDFDALK
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                                                                                                                                                                                     present sequence represents Agrobacterium tumefaciens catalase
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71.0%; Pred. No. 6.8e-236;
iive 86; Mismatches 121;
                                                                                                                                              English.
                                                                                                                                            Disclosure; Page 63-67; 70pp;
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Matches 508; Conservative
                                                                                                             ROS-inducible promoter
2002-643421/69
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                                                                                                                                                                                                                                                                                                                               MIRMAMHSAGTYRIADGRGGGGGGGGGGRFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISW
                                                                                      ADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPET
                                                                                                        MENPLAAVQMGLIYVNPEGVNGHPDPLRTAQQVLETFARMANDEKTAALTAGGHTVGNC
                                                                                                                                                                                HGNGNASALAPDPKASDVENGGLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYFDL
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H2O2 level; antioxidant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of Agrobacterium tumefaciens catalase KatA gene
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274 LETFARMAMNDEKTAALTAGGHTVGNCHGNGNASA-LAPDPKASDVENQGLGWGNPNMQG 332
                         252 RETFGRMANNDEETVALIAGGHTFGRTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTG 311
                                                                                                                                                                        431
                                                                                                                                                                                                                       GSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWQKKEYVVKPE 620
                                                                                                                                                                                                                                                                                                                                                                        611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WK--PVGSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVYAQDDNGEKFVRDFVA 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMLYDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTK
                                                                     333 KASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHHWEPIDIKKENKPVDA
                                                                                                                                        SDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRY
                                                                                                                                                                                                       IGPEVPAEDLIWQDPIPAGNTDYCE----EVVKQKIAQSGLSISEMVSTAWDSARTYRGS
                                                                                                                                                                                                                                                                       DMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQISAD-----TGASIADVIVLA
                                                                                                                                                                                                                                                                                                                                                                                                         EMLLDRAQLAGLTGPENTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoniazid resistance; restriction fragment length polymorphism;
RTFP, katG gene; catalase; paroxidase; multiple drug resistance:
Isonicotinic ecid hydrazide; IRH; tuberculosis; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "mutation to Thr confers INH resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to Thr confers INH resistance'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "mutation to Cys confers INH resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "mutation to Leu confers INH resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis wild-type catalase-peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW26596 standard; Protein; 740 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0418782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0418782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          739 AWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732 AWAKVMDLDRFDL 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is of the Microscilla furvescens catalase-53CAI.

Cutalase-73CAI may be used to catalyse oxidation reactions such as epoxidation or hydroxylation. The enzyme can also be used to detect to describe hydrogen percutale, e.g. in connection with glyoxylic acid preduction. Discensors, contact lass cleaning, pulpydaper bleaching and parternisation of darry products. Antibodies realised against producting and purification of calls containing the enzyme. Prespects to the gene product as a cargine. Frespects of the gene encoding catalase-53CAI can be used to identify related sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGGGGRAPLNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 GKCPVMHGG---NTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 DIYWGDEKEWLAPSDERY-GDVNKPETMENPLAAVONGLIYVNPEGVNGHPDPLRTAQQV
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or
                                                                                                                                                                                                                                                  Catalase: epoxidation; hydroxylation; biosensor; paper bleaching;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Now bacterial cataleses, related nucleic acid vectors and transformed cells "used as oxidising, agents and for detecting destroying hydrogen peroxide, e.g. in blosensors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.4%; Score 2290.5; DB 19; Length 745; 59.1%; Pred. No. 7.8e-190; 1.ve 92; Mismatches 183; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanyal I;
                                                                                                                                                                                                                  Microscilla furvescens catalase-53CA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RECO-) RECOMBINANT BIOCATALYSIS INC
                                                                                                                   Ź
                                                                                                                   AAW33810 standard; Protein; 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adhikary RS, Robertson DE,
                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US16513.
                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0674887
                                                                                                                                                                                  18-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433; Conservative
                                                                                                                                                                                                                                                                                                   Microscilla furvescens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-086953/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       745 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV06555
                                                                                                                                                                                                                                                                     pasteurisation.
                                                                                                                                                                                                                                                                                                                                 WO9800526-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                    08-JAN-1998
                                899
                                                                                                                                                    AAW33810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                     AAW3381
                                                                                   RESULT
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The invention realites to a novel method of detecting Mycobacterium to theoremists. The method comprises amplifying the DMA in the samples to generate a detectable amount of amplified DMA comprising a catalase. Provide (Rut) DMA fragment with sequence of bases 904-1530 of the PMA tuberculosis strain H37PW MX katG gene sequence. The method optionally truberculosis strain H37PW MX katG gene sequence. The method optionally threcoilion mutation in coden 315 (83197 mutation), indicative of an consorting act of hydraxide (IMN) resistant W. tuberculosis strain. The method can be used to detect M. tuberculosis in this disease is a major count of the depends on identification of the ctologic agent M. tuberculosis. This disease is a major cause of human morbidity and mortality, and conclusive disposais of M. tuberculosis is the disposal of method can be identified the been used in tuberculosis treatment but strains have amerged; the method allows such drug-resistant strains to be identified. The present sequence represents the wild-type M. tuberculosis kind gene product.
  533 PGNIKVSFADLVVLGGCAAIEKAAKAAGHNITVPFTPGRTDASQEQTDVESFAVLEPKAD 592
                                                                                                                                                              Catalase-peroxide; katG; mutant; mutation; isonicotinic acid hydrazide; INH; tuberculosis; diagnosis; detection.
                                                                    GFRNWQKKEYVVKPEEMLLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQ
                                                                                                                                   LTNDFFVNLTDMGNSWK--PVGSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20; Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of Mycobacterium tuberculosis - by amplifying kato and detecting specific fragment, and optionally identifying INN-reasistant strains by detecting specific mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 50.4%; Score 2044;5; DB 20; Length Best Local Shallarity 54.3%; Pred: No. 1.9e-168; Matches 20; Conservative 93; Mismatches 220; Indels Matches 20; Conservative 93; Mismatches 220; Indels

    M. tuberculosis catalase peroxide (katG) gene product.

                                                                                                                                                                                                                       724 AQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                               AAW95398 standard; Protein; 740 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 7; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US09285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sockerill FR, Kline BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-070099/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           740 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX00817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09850585-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 VNGHPDPLRTAQQVLETFARMANDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 NQGLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHHWE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 AKDGAGAGIIPDPFGGPG--RSPTMLATDLSLRVDPIYERITRRWLEHPEELADEFAKAW 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEEV----VKQKIAQSGLSISEM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSTAMDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPE-RLAKVLSVYEQI----SAD 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TG---ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLAD 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID-IKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 VSPRHRAIRER---AMSGKCPVM-HGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFNYREEVRKLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTTRIADGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPETMENPLAAVQMGLIYVNPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGFGFGRVDQWEPD-EVYWGKEATWL--GDERY----SGKRDLENPLAAVQMGLIYVNPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thererousts wild-type catalase proxidase enzyme. Claimed methods of rapidly identifying strains of w. tuberculosis which are believed to the tuberculosistic during its tuberculosis which are believed to the tuberculosistic during isoniard (INH) are based on (see Any8040) that confer INH resistance and which coincidently stess. In the addition or deletion of restriction endouclease sistes. Finants (see Any80401-02) are provided for the PCR and publication of a katig gene from a test W. tuberculosis strain, and further primers (see Any80401-05) for use in the restriction fragment length polymorphism analysis of the amplified gene and hence determination of the susceptibility to INH of the strain.
                                                                                                                                                                                            Determining susceptibility of Mycobacterium tuberculosis strains to isoniazid - by detecting mutation(s) in the catalase-peroxide gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 18; Length 740;
                                                                                                                                                                                                                                                                                                                          this polypeptides comprises a consensus of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 2044.5; DB 18; Pred. No. 1.9e-168; 93; Mismatches 220;
                                                                                                                                                                                                                                                                             Example 2; Column 31-36; 38pp; English.
                                                                                      ä
                                                                                      THD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.4%;
  94US-0228662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 54.3%
Matches 406; Conservative
                                                                                   Cockerill FR, Kline BC,
                                         (MAYO-) MAYO FOUNDATION
                                                                                                                                1997-424226/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                740 AA;
                                                                                                                                                  N-PSDB; AAT90400
18-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      £13
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us-09-884-889-6.rag

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This protein sequence represents the consensus amino acid sequence of the sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRDMGPVARYLGPLVPKQTLLWQDPVPAVSHDLVGEAEIASLKSQIRASGLTVSQLVSTA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 REEVRKLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRWAWHSAGTYRIADGRGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 AGAGTIPDPFGGFG--RSPTMLATDLSLRVDPIYERITRRWLEHPEELADEFAKAWYKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRDLGPKSRYIGPEVPAEDLIWODPIPAGNTDYCEEV----VKQKIAQSGLSISEWVSTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRAIRER---AMSGKCPVM-HGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPPITETTTGAASNGCPVVGHMKYPVEGGGNQDWWPNRLNLKVLHQNPAVADPMGAAFDY
                                                                                                                                                                                                             tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19; Length 740;
                                                                                                                                                                                                     Determination of isoniazid sensitivity of Mycobacterium tuberc
strains – by restriction length polymorphism analysis of katG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.3%; Score 2041.5; DB 19
Best Local Similarity 54.4%; Pred, No. 3.5e-168;
Best Local Similarity 54.4%; Pred, No. 3.5e-168;
Best Local Similarity 54.4%; Pred, No. 3.5e-168;
                                                                                                                                                                                                                                                                 Example 2; Column 15-20; 18pp; English.
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94US-0228662
                                       94US-0228662
                                                                                                                     Cockerill FR, Kline BC,
                                                                               (MAYO-) MAYO FOUNDATION
                                                                                                                                                               WPI; 1998-007975/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           740 AA;
18-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                NOCLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHFWE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494
                                                                                                                       VSPRHRAIRER---AMSGKCPVM-HGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDP
                                                      VPEOHPP ITETTTGAASNGCPVVGHMKYPVEGGGNQDWPNRLNLKVLHONPAVADPMGA
                                                                                                 DFNYREEVRKLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRG
                                                                                                                                                                                                                                                                 YGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPETMENPLAAVOMGLIYVNPEG
                                                                                                                                                                                                                                                                                       VNGHPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVE
                                                                                                                                                                                                                                                                                                                                                                                        PNGNPDPMAAAVDIRETFRRMAMNDVETAALIVGGHTFGKTHGAGPADLVGPEPEAAPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMGLGWKSSYGTGTGKDAITSGIEVVWTNTPTKWDNSFLEILYGYEWELTKSPAGAWQYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 PID-IKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEEV----VKQKIAQSGLSISEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSTAWDSARTYRGSDMRGGANGARIRLAPONEWOGNEPE-RLAKVLSVYEOI----SAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TG---ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGNIKVSFADLVVLGGCAAIEKAAKAAGHNITVPFTPGRTDASQEQTDVESFAVLEPKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFRNWQKKEYVVKPEEMILDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINDFFVNLTDMGNSWK--PVGSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis katG protein consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculosis, katG gene; isoniazid resistance; isonicotinic acid hydrazide; consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 724 AQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW31343 standard; Protein; 740 AA
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Fri Oct 10 11:39:14 2003

Length 740;

DB 20;

740 AA;

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Sequence
                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention realies to a novel method of detecting Mycobacterium to the invention realies to a novel method of detecting Mycobacterium to the the comprises a mapified the DNA in the samples to generate a detectable amount of amplified DNA comprising a catalase.

Exercise (Kato) DNA fragment with sequence of Dases 904-1533 of the PNA to the Comprising a catalase.

Exercise (Kato) DNA fragment with sequence. The method optionally the tuberculosis strate in 178 Was ketting of the Acto DNA fragment has a serine to threcoine mutation in codon 315 (3313T mutation), indicative of an conclusive catal Mydrated (TNN) resistant W tuberculosis strain. The method can be used to detect W. tuberculosis in biological fuluds, and subsequent treatment depends on identification of the ethologic agent M. tuberculosis. This alsease is a major cause of human morbidity and mortality, and conclusive diagnosis of Mr suberculosis. The although a major cause of human morbidity and mortality, and conclusive diagnosis of Mr tuberculosis. The although agent of the thought of the Mr tuberculosis the mino acid strains to be identified. The present sequence represents the mino acid strains to be identified. The present sequence represents the mino acid conclusive the Mr tuberculosis trains.

Exercise the Mr tuberculosis kind gene product given in Fig 7.
                                                          727
                                                                        WORKEYVVRPEEMLLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTND
                                                          FFVNLTDMGNSWK - - PVGSNAYEIRDRRTGAVRWTASRVDLVFGSNSLLRSYAEVYAQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of Mycobacterium tuberculosis - by amplifying katG gene
and detecting specific fragment, and optionally identifying
TRH-resistant strains by detecting specific mitation
                                                                                                                                                                                                                                                                                                                                      Catalase-peroxide; katG; mutation; isonicotinic acid hydrazide;
                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- S315T
/note= "wild-type Ser is replaced by Thr"

    M. tuberculosis catalase peroxide (katG) gene variant.

                                                                                                                                                                                                                                                                                                                                                    INH; tuberculosis; diagnosis; detection; variant.
                                                                                                                                   116 AQPKFVQDFVAAWDKVMNLDREDV 739
                                                                                                                 728 NGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                              Key Location/Qualifiers
Misc-difference 315
                                                                                                                                                                                                                  AAW95399 standard; Protein; 740 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0852219
                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSTAWDSARIYRGSDMRGGANGARIRLAPQNEWQGNEPE-RLAKVLSVYEQI----SAD 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQGLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHHWE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 AKDGAGAGTIPDPFGGPG--RSPIMLATDLSLRVDPIYERITRRWLEHPEELADEFAKAW 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          439 FKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEEV----VKQKIAQSGLSISEM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 TG---ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLAD 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFRNWQKKEYVVRPEEMLLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQ 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 GFRNYLGKGNPLPAEYMLLDKANLLTLSAPEMTVLVGGLRVLGANYKRLPLGVFTEASES 652
                                                                                                     79
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                                                                                                                          1 VPEQHPPITETTTGAASNGCPVVGHMKYPVEGGGUQDWWPNRLNLKVLHQNPAVADPMGA
                                                                                                                                                                                                             235 PNGNPDPMAAAVDIRETFRRMAMNDVETAALIVGGHTFGKTHGAGPADLVGPEPEAAPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 VSPRHRAIRER - - - AMSGKCPVM - HGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDP
                                                                                                                                                                                    DPNY REEVRKLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRWAWHSAGTYRIADGRG
                                                                                                                                                                                                                                                                                                                                                                YGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPETMENPLAAVQMGLIYVNPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 PID-IKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINDFFVNLIDMGNSWK -- PVGSNAYEIRDRRTGAVKWTASRVDLVFGSNSLLRSYAEVY
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catalase-peroxidase; isonicotinic acid hydrazide; isoniazid; INH; antiblotic; susceptibility; sensitive; resistant; katG.
                                                       Indels
50.3%; Score 54.1%; Pred. No. 3.De-zz.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.tuberculosis H37Rv catalase-peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR43670 standard; Protein; 735 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                              Local Similarity 54.1% tes 405; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                                                                                                             140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR43670;
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552
                                                                                                                                                                                                                                                                       672
    441
                                                                                                                                                                                                                                                                                                                                                           383 -IKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKL
                                  357 GAGAGTIPDPFGGPG--RSPTMLATDLSLRVDPIYERITRRWLEHPEELADEFRKAWYKL
                                                                     THRDLGPKSRYIGPEVPAEDLIWQDPIPA-GNTDYCEEV--VKQKIAOSGLSISEMVSTA
                                                                                                    415 IHRDMGPVARYLGPLVPKOTLLWQDPVPAVSTTSSAKQIASLKSQIRASGLTVSQLVSTA
                                                                                                                                    WDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQIS-----ADTGAS
                                                                                                                                                                                                      IADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWQK
                                                                                                                                                                                                                                                                       KEYVVKPEEMLLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFV
                                                                                                                                                                                                                                                                                                     KGNRCRPSTSLLDKANLLTLSAPEMTVLVGGLRVIGANYKRLPLGVFTEASESLTNDFFV
                                                                                                                                                                                                                                                                                                                                        NLTDMGNSWR--PVGSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVYAQDDNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding catalase-peroxidase HPI - useful for rapid identification of isoniazid resistant Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the catalase-peroxidase enzyme encoded by the grobacterium tuberculosis AttG gene. The gene was soluted from a M. tuberculosis strain resistant to isonicothic acid hydraxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (atG; catalase; peroxidase; enzyme; isonicotinic acid hydrazide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoniazid; INH; diagnosis; resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10A; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW78363 standard; Protein; 735 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          731 KFVRDFVAAWTKVMNADRFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÖB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0459499.
92US-0875940.
92US-0929206.
93US-0029655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.tuberculosis katG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDICAL RES COUNCIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UYPA-) UNIV PARIS VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-166622/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole ST, Heym B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX16963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-2003
11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5871912-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-1995:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPRASDVENQG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGWGNPNWQGKASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHHWEPID 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHRAIRER----AMSGKCPVM-HGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QHPPITETTTGAASNGCPVVGHMKYPVEGGGNQDWWPNRLNLKVLHQNPAVADPMGAAFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGSQRFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GGMORFAPLNSWPDNASLDKARRLLWPVKKKYGKKLSWADLIVFAGNRCARNRWASRRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPDPMAAAVDIRETFRRMAMNDVETAALIVGGHTFGKTHGAGPADLVGPEPEAAPLEQMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFGRVDIWEPEKDIYMGDEKEWLAPSDERYGDVNKPETMENPLAAVQMGLIYVNPEGVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Match gene of Mycobacterium tuberculosis was isolated on a KpnI framment by shocking the sequence contrains one open reading framme with high coding probability; a 735 amino acid protein is encoded by the form high coding probability; a 735 amino acid protein is conformed by the form high coding probability; a 735 amino acid protein is conformed to the structure of known bacterial catalase-proxidases which consist of two modines (possibly the result of a duplication event), both showing hamology to the yeast enzyme, fised to a unique the katch gene can result in loss of IRM succeptibility, i.e. the formation of an inhority castering wycobacterial strains (popaged on 32-WAR-2003 to correct PM field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Rapid detection of antibiotic resistance in Mycobacteria - esp. isoniazid, rifampicin or streptomycin resistance in tuberculosis by detecting mitation in ketG, rpoB or rpsi, genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 735;
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                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.6%; Score 1890; DB 14;
51.3%; Pred. No. 5.1e-155;
ive 95; Mismatches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14;
                                                                                                                                                                                                                                                                                                                      Telenti
Mycobacterium tuberculosis (strain H37Rv).
                                                                                                                                                                                                                                                                                                                   Honore N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV BERNE.
UNIV CURIE PARIS VI P & M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 8; 97pp; English.
                                                                                                                                92US-0815940.
92US-0875940.
92US-0929206.
93FR-0004545.
                                                                                                                                                                                                                                                                                                                   Heym B,
                                                                                                 93WO-EP01063
                                                                                                                                                                                                                    (ASSI-) ASSISTANCE PUBLIQUE.
                                                                                                                                                                                                                                                  MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 51.3%
Matches 380; Conservative
                                                                                                                                                                                                                                      INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                  1993-368812/46.
                                                                                                                                                                                                                                                                                                                   Cole S,
Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           735 AA;
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ51531
                                WO9322454-A1
                                                                                                 30-APR-1993;
                                                                 11-NOV-1993
                                                                                                                                  17-SEP-1992;
                                                                                                                                                                                   16-APR-1993;
                                                                                                                                                10-APR-1992
                                                                                                                                                                   14-AUG-1992
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                                                                                                                                                                                                                                                                                                                                    foung D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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LDYWALKEDLRKIMTESQDWWPADYGHYGPLFIRMAWHSAGTYRIADGRAGASTGTQRFA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWITKSPACAWOWMAVDPDEKDLAPDAEDPSKKVPTWMMTTDLALREDPEYEKIARRFHO 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 KILNSGLTVSELVKTAWASA-ARSATRISAATNGRRIRLAPQKDWEVNEPERLAKVLSVL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512 RGHPARTA-------EKSKHR-----RLDRLGGTLRWKRQPATPALMSNCHF 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 QNRQNAAQCPFHESVTNQSSNRTTNKD#WPNQLNLSILHQHDRKTNPHDEEFNYAEEFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGF--SFGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 YVNPEGVNGHPDPLRTAQQV-----LETFARMAMNDEKTAALTAGGHTVGNCHGNGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NGVNLR-OPRRAGROASKSRGISAETFRRMGMKDEETVALIAGGHTFGKAHRGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WELKKSPAGAHHWEPIDIKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPEYFKKTFAKAWFKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCE---EVVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 RERAMSGKCPVMHG--GNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 LDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGSQRFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLNSSPDNANLDKARRCYGRSKRNTGTK-----SLG-PICSFWRAMSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIWEPE-------KDIYWGDEKEWLAPSDERYGDVNKPETMENPLAAVQMGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRWVEKRLDSAAGPLTSCIRKKTFIGDRKKSGSPLNAI--PVIATSKTRSPRA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIAQSGLSISEMVSTAWDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVLSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQISADTGASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKG-----RGDATAEMTDADSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                            DNA conty. genetic information of heat resistant peroxidase -
peroxidase by culturing transformant and collecting heat resistant
peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                               Heat resistant peroxidase may be produced from a plasmid pobl0 transformed E.coli UM228 expression system efficiently and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 38.1%; Score 1547; DB 11; al Similarity 43.9%; Pred. No. 3.4e-125; 342; Conservative 89; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 8pp; Japanese.
                                                          Bacillus stearothermophilus
                                                                                                                                                           89JP-0089469
                                                                                                                                                                                            89JP-0089469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     in large quantities.
                       poD10; E.coli UM228.
                                                                                                                                                                                                                                                           WPI; 1990-372008/50.
N-PSDB; AAQ06815.
                                                                                                                                                                                                                            (TOYM ) TOYOBO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      731 AA;
                                                                                         JP02268684-A
                                                                                                                                                           07-APR-1989;
                                                                                                                                                                                            07-APR-1989;
                                                                                                                            02-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Matches
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                                                                                                                                                                                                                                                                           64 YAAEVATSRLDALTRDIEEVMTTSQPWWPADYGHYGPLFIRMAWHAAGTYRIHDGRGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FADLVVLGGCAPLEKAAKAAGHNITVPFTPGPHDASQEQTDVESFAVLEPKADGFRNYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 RHRAIRER---AMSGKCPVM-HGGNISTGTSNKDWWPEGLNLDILHOQDRKSDPMDPDFN
                                                                                                                                                                                                                     OHPPITETTTGAASNGCPVVGHMKYPVEGGGNQDWWPNRLNLKVLHONPAVADPMGAAFD
                                                                                                                                                                                                                                                         83 YREEVRKLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGG
                                                                                                                                                                                                                                                                                                                          143 TGSQRFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGF
                                                                                                                                                                                                                                                                                                                                                           124 GGMORFAPLNSWPDNASLDKARRILIWPVKKYGKKLSWADLIVFAGNRCARNRWASRRSG
                                                                                                                                                                                                                                                                                                                                                                                               SFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPETMENPLAAVQMGLIYVNPEGVNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 GAGAGTIPDPFGGPG--RSPTMLATDLSLRVDPIYERITRRWLEHPEELADEFRKAWYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THRDLGPKSRYIGPEVPAEDLIWQDPIPA-GNTDYCEEV--VKQKIAQSGLSISEMVSTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      553 IADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYVVKPEEMLIDRAQLMGLIGPEMTVLLGGMRVLGINIGGIKHGVFTDCEGQLINDFFV
                                                                                                                                                        Gaps
(isoniazid or INH). The sequence is useful in the diagnosis of tuberculosis caused by INH-resistant M. tuberculosis and in the identification of other INH-resistant strains. (Updated on 20-MMR-2003 to correct PA field.)
                                                                                                                                                        26;
                                                                                                                          Length 735;
                                                                                                                                                        Indels
                                                                                                                       Score 1890; DB 20;
Pred. No. 5.1e-155;
95; Mismatches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat resistant peroxidase gene product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR08205 standard; protein; 731
                                                                                                                       46.6%;
llarity 51.3%;
Conservative 95
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                                                                                                                                     Similarity
                                                                                      735 AA;
                                                                                                                                                      380;
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                                                                                         Sequence
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350 PTKFDMGYFDLLFGYNWELKKSPAGAHHWEPIDIKKENKPVDASDPSIRHNPIMTDADMA 409
                                                                                                                                                                                                                                                                                                                              IKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPEVPAEDLIWQDPIP 469
                                                                                                                                                                                                                                                                PTOWSNYFFENLFKYEWVQTRSPAGAIQFEAVD-APEIIP-DPFDPSKKRKPTMLVTDLT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                            470 AGNTDYCEEVV---KOKIAQSGLSISEMVSTAWDSARTYRGSDMRGGANGARIRLAPQNE 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 QPIYNPTEQDIIDLKFAIADSGLSVSELVSVAWASASTFRGGDKRGGANGARLALMPQTR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 TGDVTRRQPIRALPVLEKIQKESGRASLADIIVLPGLEVVEKSASAAGLSIHVPFAPGRV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 DATAEMTDADSFAPLEPLADGFRNWQKKEYVVKPEEMLLDRAQLMGLTGPEMTVLLGGMR 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 DARQDQTAIGMFELLEPIADGFRNYRARLDVSTTESLLIDKAQQLTLTAPEMTALVGGMR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  646 VLGINYGGTKHGVFTDCEGQLINDFFVNLTDMGNSWRPV--GSNAYEIRDRKTGAVKWTA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 WQGNEPERLAKVLSVYEQISADTG-ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRG
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food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                  ä
                                                                                         Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     704 SRVDLVFGSNSLLRSYAEVYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                 25.9%; Score 1050; DB 22;
52.9%; Pred. No. 3.4e-82;
ive 58; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 39182; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
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23-AUG-2000; 2000US-0649167.
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                                                                                                              Best Local Similarity 52.99
Matches 216; Conservative
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                            533 AA;
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                            Sequence
                                                                                     Query Match
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                                                                             552 SLAAAMRHKSKPMSKALPCWNRSQMASATIKSKSTRFRRKSCSSTKPSSS-ADRPRNDGL 610
                                                                                                                                      633 TGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWRPVGSNAYEIR 692
                                                                                                                                                                                                   611 SWRFARV ----- GPNYRHLPHGVFTDRIGVLTNDFFVNLLDMNYEWVPTDSGIYEIR 662
                                                                                                                                                                                                                                                            693 DRKTGAVKWTASRVDLVFGSNSLLRSYAEVYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                             A-----PLEPLADGFRNWQKKEYV------VKPEEMLLDRAQLMGL
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #25048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG25057 standard; Protein; 533 AA.
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23-AUG-2000; 2000US-0649167.
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                                The invention leaders to solute up to high actions to proper the component of the component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 KOKTAQSGLSISEMVSTAWDSARTYRGSDWRGGANGARIRLAPQNEWQGNEPERLAKVLS 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 VLEKIOKESGKASLADIIVLAGVVGVEKAASAAGLSIHVPFAPGRVDARODOTDIEMFEL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDCEGQLTNDFFVNLTDMGNSWRPV - - GSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLR 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 VYEQISADIG-ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 273;
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                      invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.3%; Score 784.5; DB 22; 58.4%; Pred. No. 1.4e-59; ive 36; Mismatches 73; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYAEVYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 AVAEVYASSDAHEKFVKDFVAAWVKVMNLDRFDL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0649167.
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Best Local Similarity
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23-AUG-2000;
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The invention relates to isolated polynuclectide (I) and and optopeptide (II) sequences. (I) is useful as hybridistation probes, polypeptide (II) sequences. (I) is useful as hybridistation probes, polynuclectides are chain recombinant production of (II). The copynuclectides are also used in diagnostics as expressed expense to polynuclectides are also used in diagnostics as expressed expense to confinity of expressed genes. (I) is useful in gene therapy rechniques to restore normal activity of (II) or to treat disease states involving or control as useful in energial as purpoperide in tissue, as molecular weight markers and as cod supplement. (II) and its binding participate against II, detecting or important protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in the polypeptide and polynuclectide sequences have applications in the prolyperide and polynuclectide sequences have applications in craponship for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences Addonoto-AB30377, represent novel human condition but was obtained in a electronic format directly from WIPO the analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 PIKFDMGYFDLLFGYNWELKKSPAGAHHWEPIDIKKENKPVDASDPSIRHNPIMTDADMA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529 PTQWSNYFFENLFKYEWVQTRSPAGAIQFEAVD-APELIP-DPFDPSKKRKPTMLVTDLT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 IKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPEVPAEDLIWQDDIP 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 AGNTDYCEEVV---KOKIAQSGLSISEMVSTAWDSARTYRGSDMRGGANGARIRLAPQNE
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                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in addinostics, forensics, gene mapping, identification of mutations aresponsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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12.8%; Score 519; DB 22;
Best Local Similarity 49.8%; Pred. No. 2.6e-35;
Marcches 107; Conservative 34; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 39656; 103pp; English.
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                                                                      Tang YT;
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                                                                      Drmanac RT, Liu C,
                                                                                                                  WPI; 2001-639362/73
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                    (HYSE-) HYSEQ INC.
                                                                                                                                          N-PSDB; AAS73484
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The invention relates to isolated polynucleotide (I) and coppepted (II) sequences. (I) is useful as hybridisation probes, colymerase chain reaction (PCR) primers, oligomers, and for chromsome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The colynucleotides are also used in disposition sequence traps to 'Or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to creatore normal activity of (II) or to treat disease states involving the activity of (II) or to treat disease states involving the activity of (II) or to treat disease states involving a polypeptide in tissue, as molecular weight markers and as the dod supplement. (II) and its binding partners are useful for treating of states expressing (II). (I) are useful for treating of adjacedist and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the disposation for genetic disorders or other traits to assess biodiversity of annino acid sequences. Associated appendent on DNA and configuration and to produce other types of data and produced dependent on DNA and configuration and to produce other types of that man produce data for the invention. One annino acid sequences Associated appendent on DNA and configuration but was obtained in electronic format directly from WIPO activity when the activity of the invention of the activity of the annino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         623 LLDRAQLMGLIGPEMIVILGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWK 682
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9.8%; Score 398; DB 22; Length 201;
Best Local Similarity 41.2%; Pred. No. 3.6e-26
Matches 89; Conservative 24; Mismatches 43; Indels 66
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23-AUG-2000; 2000US-0649167
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                                                                                    WO200175067-A2.
           Homo sapiens.
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Search completed: October 7, 2003, 19:42:20 Job time : 64.8231 secs

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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:40:18 ; Search time 22:1175 Seconds (without alignment) 140:492 Million cell updates/sec

11tle: US-09-884-889-6 Perfect score: 4058

Perfect score: 4058 Sequence: 1 MNNASADDLHSSLQQRCRAF.....RDFVAAWTKVMNADRFDVAS 753

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters:, 328717

328717 seqs, 42310858 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by an anysis of the total score distribution.

## SUMMARIES

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NO.	Score	Match	Length DB	DB	a.	Description	ä	
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n	2290.5	56.4	745	m	US-08-951-844-8	Sequence	<b>6</b>	Appl
9	2290.5	56.4	745	4	US-09-412-347-8	Sequence	œ,	App1
7	2093	51.6	726	7	US-08-313-185-49	Sequence	49	App
80	2093	51.6	726	~	US-08-459-499-13	Sequence	13,	
σħ	2093	51.6	726	m	US-09-082-614A-49	Sequence	49,	
10	2072.5	51.1	726	4	US-09-328-352-8115	Sequence	811	
11	2044.5	50.4	740	-	US-08-418-782-21	Sequence	21.	App
12	2044.5	50.4	740	~	US-08-852-219-21	Sequence	21,	
13	2041.5	50.3	740	П	US-08-418-782-7	Sequence	1,	App1.
14	2041.5	50.3		-	US-08-228-662-7	Sequence	,	Appl
15	2041.5	50.3		~	US-08-852-219-7	Sequence	7,	Appl
16	2040.5	50.3		ď	US-08-313-185-50	Sequence	20,	App
17	2040.5	50.3		~	US-08-459-499-14	Sequence		App
18	2040.5	50.3		E	US-09-082-614A-50	Sequence		App
19	1890	46.6		7	US-08-313-185-48	Sequence	48,	App
2	1890	46.6	735	~	US-08-459-499-9	Sequence		Appl
21	1890	46.6		e	US-09-082-614A-48	Sequence		App
22	1885	46.5		~	US-08-459-499-12	Sequence		App
23	1681	41.4		ď	US-08-313-185-53	Sequence	53,	App
24	1681	41.4		7	US-08-459-499-17	Sequence	17,	App
25	1681	41.4		٣	US-09-082-614A-53	Sequence	53,	App
56	1616	39.8	731	N	-185	Sequence	21,	App
27	1616	39.8	731	~	US-08-459-499-15	Sequence	15,	App

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Query Watch

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Best Local Similarity 100.0%; Pred. No. 0;

Maches 73; Conservative 0; Mismatches 0; Indels 0; Gaps

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APPLICATION NUMBER: US/08/951,844
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Matches 753; Conserv
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                                                                                                                        MIRMAWHSAGTYRIADGRGGGTGSQRFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISW
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NUMBER OF SEQUENCES: BAIN, GILFILLAN,
ADDRESSEE: CACCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITT: ROSELAND
STATE: NUMBERS OF STREETS
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Patent No. 6074860
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                 ,0; Mismatches
                                                                                                                                                                                                                                                                                                                                  100.0%; Score 4058;
100.0%; Pred. No. 0;
                                                                                                                        331400-55
                               APPLICATION NUMBER: 08/674,887
FILING DATE: July 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                   REFERENCE/DOCKET NUMBER: 3314
TELECOMONICATION INFORMATION:
TELEPRONE: 201-94-1706
TELEPRONE: 201-94-1706
INFORMATION FOR EGG ID NO: 6:
SEQUENCE CHARACTERICS:
LENGTH: 753 AMINO ACIDS
TIPE: AMINO ACID
                                                                                                       28,019
                                                                                                                                                                                                                                                                               MOLECULE TYPE: Polypeptide
                                                                                    NAME: Charles J. Herron
REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                   753; Conservative
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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Qy 301 HGNGNASALAPDPKASDVBNGCLGWGNPNNQGRASNAVTSGLEGAWTYNPTKFDMCYFDL 360	09   361 LFGYRWELKKSPAGAHHWEPIDIKKENKPUDASDPSTRHNFIMTDADMAIKVNPTYRALG 420	0y   601 EPLADGERHWOKEEVVVRPEMILIDRAQLMGLTGPEMTVL.GGRRVGGTRHGVFT 660	RESULT 4  UG-674-897A-8  UG-674-897A-8  Sequence B, Application US/06674897A  PATEUT S. S339100  APPLICANT: Sonyal, Industit  APPLICANT: Sonyal, Industit  APPLICANT:	COUNTRY: US  ZIP: 92037  ZIP: 92037  COMPUTER: LIBACCHE SOFTWARE: FASTENA CHARLE: MAINORANGE: US/08/674,887A  FILING DAME: 03-JUL-1996 FILING DAME: 03-JUL-1996 FILING DAME: NUMBER: 187  APPLICATION NUMBER: 188  ATOCNET MAINER: 181-0, Lisa A. RESISTRATION NUMBER: 09015/002001 TELECOMMUNICATION INFORMATION:	; INFORMATION FOR SEQ ID NO: 8: ; SEQUENCE CHARACTERISTICS:
Qy 721 EVYAQDDNGEKEVRDFVAAMTKVMNADREDVAS 753 		STATE: CA COUNTRY: US TIP: 90371 COMPUTER READBLE FORM: COMPUTER READBLE FORM: COMPUTER: IDSACRET COMPUTER:	ATORNEY AGENT HYPORANTION: NAME: Halle, Ph.D., Lisa A. NAME: Halle, Ph.D., Lisa A. REGISTRATION WHERE: 38,347 REFERENCE COCKET NUMBER: 0915/002001 TELECOMMUCATION INTORNATION: TELECOMMUCATION FOR SED 10: SEQUENCE TRANCETERISTICS: SEQUENCE TRANCETERISTICS: SEQUENCE TRANCETERISTICS: TYPE: Annio acid TOPOLGOY: linea acid TOPOLGOY: linea acid TOPOLGOY: linear brotein FRAGMENT TYPE: internal US-09-412-347-6	Query Match         100.04; Score 4058; DB 4; Length 753;           Bast Local Similarity         100.04; Score 4058; DB 4; Length 753;           Matches         753; Conservative         0; Mismachobes         0; Indels         0; Gaps         0;           OY         MNNAGADDLESSLOGRCRAFVPLVSPRIBATERBANGGKCPWHGGNFSTGTSNKDWFPE 60         1         1         1           Db         1 MNNAGADDLESSLOGRCRAFVPLVSPRIBATERBANGGKCPWHGGNFSTGTSNKDWFPE 60         0         1         1           OY         61 GLNLDLEHGODRKSDPMDPDFNYREEVEKLDFDALKKUVHALMTDSGEWMPADMGHYGGL 120         0         1         1           Db         61 GLALLIGOODRKSDPMDPDFNYREEVEKLDFDALKKUVHALMTDSGEWMPADMGHYGGL 120         0         1         1           OY         121 MIRWAMBSGTYRIADGRGGGGTGSGNFAPLNSWPDNYSLDKARRLAMPIKKKYGRKISW 180         0         0         1           Db         121 MIRWAMBGATYRIADGRGGGGTGSGNFAPLNSWPDNYSLDKARRLAMPIKKKYGRKISW 180         0         1         1           OY         121 MIRWAMGATYRISMGLEAYCESGRRAPHNSWPDNYSLDKARLLAPSKKKKKKKKKIN 180         0         0           OY         181 ADLMILAGTYRISMGLEAYCESGRRAPHNSWPDNYSLDKRARLAPSDRYCKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	Qy 241 MENDLAAVQMGLIYVNPEGVNGHPDPLRTAQQVLETFARMANDEKTAALTAGGHTVGNC 300

us-09-884-889-6.rai

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DMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQISAD-----TGASIADVIVLA 560
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                                                                                                                                  SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,844
                                                                                                                                                                                              CLÁSTIP TOMTION 435

NELOCATION PORTA: 08/674.887

PELICOCATION NUMBER: 08/674.887

RICHER DATE: 011/9. 15/66

ATTORNET AND TOMENTON:

NESSISTATION NUMBER: 28/019

RESISTENCE OF TOMENTON:

TELECOMMUNICATION TOPORATION:

TELECOMMUNICATION TOPORATION:

TELECOMMUNICATION TOPORATION:

TELEPHONE: 20.1.994.1744
                                                                                    3.5 INCH DISKETTE
                                                                                              CONDUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 745 AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 59.19
Matches 433; Conservative
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                    NEW JERSEY
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
    ROSELAND
                                                                                                                                                                                     FILING DATE:
                                                    07068
                                    COUNTRY:
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                                                                                                    Gaps
                                                                                                    25;
                                                                  DB 2; Length 745;
                                                                Query Match 56.4%; Score 2290.5; DB 2; Length 7 Best Local Similarity 59.1%; Pred. No. 1.8e-207; Misches 433; Conservative 92; Mismatches 183; Indels Mutches 433; Conservative 92; Mismatches 183; Indels
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EPICATION 6074860
GENERAL INFORMATION:
APPLICAMIR: ROBERTSON et al.
TITLE OF INVENTION: Catalases
NUMERS OF SEQUENCES: 8
CORRESPONDENCES. 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELIA, BYRRE, BAIN, GILFILLAN, ADDRESSEE: CACCHI, STRARAT & OLSTEIN
STREET: 6 BUCKER FRAM RAAD
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                    interna
) MOLECULE TYPE: '
; FRAGMENT TYPE:
US-08-674-887A-8
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                                                                                                                            333 KASNAVISGIEGAWITNPIKFDMGYFDLLFGYNWELKKSPAGAHHWEPIDIKKENKPVDA 392
                                                                                                                                                                                                                                            393 SDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRY 452
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                                                         561 GSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWQKKEYVVKPE
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                                   215 DIYWGDEKEWLAPSDERY-GDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPLRTAQQV
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APPLICANT: Young Tooquias
APPLICANT: Thoroft Nadios
APPLICANT: Honore, Nadios
APPLICANT: Honore, Nadios
APPLICANT: Telmore, Thomas
APPLICANT: Podmer, Thomas
TITLE OF TWORTHON: Rapid Detection of Antibiotic Resistance
TITLE OF TWORTHON: In Ayrobacterium Tuberculosis
NORGEN OF SEQUENCES: 66
NORGENOUNCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/313,185
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Patent No. 5851763
GENERAL INFORMATION:
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APPLICANT: Cole, Stewart
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COMPUTER READABLE FORM:
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US-08-313-185-49
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                                                                                                                       LKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGGGGRAPLNSW 154
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552 GCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAE 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 GKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKKLDLAA 77
                                                    EMLLDRAQLMGLTGPENTVLLGGMRVLGTNYGGTRHGVFTDCEGQLTNDFFVNLTDMGNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.4%; Score 2290.5; DB (59.1%; Pred. No. 1.8e-207; iive 92; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                     AUNESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 STREE: CA John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09015/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/412,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/674,887
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Robertson, Dan E. APPLICANT: Sanyal, Indiallit. APPLICANT: Adhikari, Robert S. TITLE OF INVENTION: CATALASES NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09412347
Patent No. 6410290
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Matches 433; Conservative
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MEDIUM TYPE: Diskette
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FRAGMENT TYPE:
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us-09-884-889-6.rai

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TITLE OF INVENTION: Nucleic Acid Probes, Sequences, and Methods
TITLE OF INVENTION: To Amen Detecting Mycobacterium Tuberculosis Resistant to Isoni
TITLE OF INVENTION: Amended)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPET 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ASADDLHSSLQQRCRAFVPLVSPRHRAIRERAMSGRCPVMHGG---NTSTGTSNKDWWPE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 STSDDIHNT------TATGKCPFHQGGHDQSAGACTTTRDWWPN 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.3 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03495.0110-03000
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FILING DATE: 30-APP-1992
PRIOR APPLICATION WIMBER: US 07/929,206
FILING DATE: 27-WAY-1992
PROF PRICATION WIMBER: US 08/929,655
PROF APPLICATION WIMBER: US 08/029,655
FILING DATE: 11-WAR-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/459,499
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     Sequence 13, Application US/08459499; Patent No. 5871912; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25.146
REPERBNC-FOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1300 I Street, N.W.
                                                                                                                                                                                                                                         APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart T.
Cole, Stewart T.
APPLICANT: Young, Douglag B.
APPLICANT: Zhang, Ying
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SEQUENCE CHARACTERISTICS:
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amino acid
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MEDIUM TYPE: Floppy
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                                                                       RESULT 8
US-08-459-499-13
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                                                                                          NAME: Meyers, Kenneth J.
REGISTRAITON NUMBER: 25,146
REFERENCE/COCKET NUMBER: 0255.0068-00000
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO. 49:
SEQUENCE CHARACTERISTICS:
                                                             ATTORNEY / AGENT INFORMATION:
12-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 726 anino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-313-185-49
                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GLNLDILHQQDRKSDPMDPDFNYREEVRKLDFDALKKDVHALMTDSQEWWPADWGHYGGL
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                                                                                                                                                                                                                                                                                                                        Length 726;
                                                                                                                                                                                                                                                                                                                        Query Match 51.6%; Score 2093; DB 3; Length 7 Best Local Sinlarity 53.4%; Pred. No. 8e-189; Matches 206; Conservative 103; Mismatches 206; Indels
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                                                   NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
REPERBACE/ONCKET NUMBER: 02356.0068-00000
TELECOMUNICATION INFORMATION: TELEPRONE: (202) 408-400
TELEPROX: (202) 408-4400
INPORMATION POS EQ. ID NO: 49: SEQUENCE GRANGTERISTICS:
  APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   LENGTH: 726 amino acids TYPE: amino acids
                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-09-082-614A-49
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                                                                                                                                            LLFGYNWELKKSPAGAHHWEPIDIKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAI 419
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APPLICANT: Olo, Stewart
APPLICANT: Olo, Stewart
APPLICANT: Dang, Douglas
APPLICANT: Dang, Ying
APPLICANT: Glonore, Nadine
APPLICANT: Glonore, Nadine
APPLICANT: Glonore, Talenas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
WINNER OF SEQUENCES: 66
WINNER OF SEQUENCES: 66
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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1: 1300 I Street, N.W.
Rashington
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 QMGLGWKSSYGTGTGKDAITSGIEVVWTUTPTKWDNSFLEILYGYEWELTKSPAGANQYT 354
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                                                                                                                                                                             APPLICANT: Cockerill, Franklin R.
APPLICANT: Klice, Bruce C.
APPLICANT: Klice, Bruce C.
TITLE OF INVENTION: Detection of Isoniazid Resistant Strains
TITLE OF INVENTION: Of M. Tuberculosis
TIMERS OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: LIBM FO. Compartito.
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                               Lundberg & Woessner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/418,782
Sequence 21, Application US/08418782 Patent No. 5658733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTONEX, FAGRAT INFORMATION:
NAME: WOOSSIACH, WARTEN D.
REGISTRATION WUMBER: 350,440
REFERENCE, DOCKET WINGER: 150,1
TELECOMMUNICATION STRONMATION:
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                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Schwegman, L
STREET: 3500 IDS Center
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612-339-3061
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-418-782-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                     US-08-418-782-21
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Best Local &
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                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT GAT'L IN THE SECON OF A BL
TITLE OF INVENTION: NOTLERC ALID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILLS OF INVENTION: BAINANNII FOR DIAANOSTICS AND THERAPEUTICS
FILLS REPREMED: GTGGG-0738
FILLS REPREMED: GTGGG-0738
CURRENT FELLING DATE: 199-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS 8115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGGGGTGSQRFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 RGGAGRGQORFAPLNSWPDNASLDRARRLIWPVRQKYGQKISWADLFILAGNIALESSGF 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 VENQGLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHH 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 VSPRHRAIRERAMSGKCPVMHGGNTST-----GTSNKDWWPEGLNLDILHQQDRKSDPM 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 WEKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEEVV---KQKIAQSGLSISEM 494
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 726;
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                                                                                                                                                                                                                                                                                                                                                                                             51.1%; Score 2072.5; D
53.2%; Pred. No. 7e-187
                                                                      Sequence 8115, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Acinetobacter baumannii
US-09-328-352-8115
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                                                  US-09-328-352-8115
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                    FKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEEV----VKQKIAQSGLSISEM 494
                                                                                    495 VSTAWDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPE-RLAKVLSVYEQI-----SAD 548
                                                                                                                                            549 TG---ASIADVIVLAGSVGIEKAAKAAGYDVRVPELKGRGDATAEWTDADSFAPLEPLAD 605
                                                                                                                                                                                                            533 PGNIKVSFADLVVLGGCAAIEKAAKAAGHNITVPFTPGRTDASOEQTDVESFAVLEPKAD 592
                                                                                                                                                                                                                                                      506 GFRNWQKKEYVVKPEEMILDRAQIMGLIGPEMIVILGGMRVLGTNYGGTKHGVFTDCEGQ 665
                                                                                                                                                                                                                                                                        LTNDFFVNLTDMGNSWK--PVGSNATEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVY 723
                                                                                                                                                                                                                                                                                                                                                      LINDFFVNLLDMGITWEPSPADDGTYQGKD-GSGKVKWTGSRVDLVFGSNSELRALVEVY 711
380 PID-IKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAW 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: COCKETII, Franklin R.
APPLICANT: COCKETII, Franklin R.
APPLICANT: Rine, Bruce C.
TITLE OF TWENTION: Detection of isoniazid Resistant Strains
TITLE OF TWENTION: Of M. Tuberculosis
UNBABR OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
MODESSEE: WHELLING, Raasch & Gebhardt, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Mueting, Raasch & Gebhardt, P.A.
F: 119 No. 5922575th Fourth Street, Ste. 203
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Fatentin Release #1.0, Version #1.25
CORRENT PAPLICATION DATA:
APPLICATION UNMERS: US/08/852,219
FILIG DATE: U7/847-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                     724 AODDINGEKFVRDFVAAWTKVMNADRFDV 751
                                                                                                                                                                                                                                                                                                                                                                                                       REPERBUCE/DOCKET NUMBER: 230.00010130
TELECOMMULICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEPAX: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/08852219 Patent No. 5922575 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Sandberg, Victoria A.
REGISTRATION NUMBER: 41,287
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MEDIUM TYPE: Floppy
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Length 740;

DB 2;

50.4%; Score 2044.5;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 NOGLGWGNPNMOGKASNAVTSGIEGAWTINPTKFDMGYFDLLFGYNWELKKSPAGAHHWE 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549 TG---ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLAD 605
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                                                                             24 VSPRHRAIRER----AMSGKCPVM-HGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDP 79
                                                                                                        235 PNGNPDPMAAAVDIRETFRRMAMNDVETAALIVGGHTFGKTHGAGPADLYGPEPEAAPLE
                                                                                                                                                                        80 DFNYREEVRKLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 PID-IKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAW
                                                                                                                                                                                                                                                                                                                                                                  200 YGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPETWENPLAAVQMGLIYVNPEG
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APPLICANT: Kilne Bruce C.
APPLICANT: Wilne Bruce C.
TITLE OF INVENTION: Detection of Isoniazid Resistant Strains
TITLE OF INVENTION: of W. Tuberculosis
NUMBER OF SEQUENCES: 22
NUMBER OF SEQUENCES: 22
                              Indels
54.3%; Pred. No. 3.20
Live 93; Mismatches 220;
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Patent No. 5658733
                              406; Conservative
      Best Local Similarity
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670 FFVNLTDMGNSWK--PVGSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVYAQDD 727
                       84 REEVRILDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSORFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFS 203
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                                                                                                                                                                                                                                        tch 50.3%; Score 2041.5; DB 1; Length 740; all Similarity 54.4%; Pred. No. 6.1e-184; Add 405; Conservative 92; Mismatches 218; Indels 29; 405; Conservative 92; Mismatches 218; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                   LUNDBERG & WOESSNER, P.A
                                                                      728 NGEKEVRDEVAAWTKVMNADREDV 751
|||:|||||| |||||| 716 AQPKEVQDEVAAWDKVMNLDREDV 739
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APPLICATION NOMBER: US/08/228,662
FILING DATE: 18-APR-1994
CLASSIFICATION: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         Sequence 7, Application US/08228662
Patent No. 5688639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY, GAGNEY INFORMATION:
NAME: MORESWIRE, MARRAR D
RELIEFRATION WIMBER: 30.440
REFERENCE/DOCKET WUMBER: 150.1)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 612-339-0331
TELECEPKX: 612-339-3361
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SEQUENCE CHARACTERISTICS:
LENGTH: 740 amino acids
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SCHWEGMAN, LU
STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS
STATE: MINNESOTA
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Best Local S
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                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,782
                                                                                                                                                                                                       150.141051
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 ATTORENY, CARENT INFORMATION:
NAME: MOGESTOR, WAITCHD D
REGIGERATION NUMBER: 30.440
REFERENCE/DOCKET VUMBER: 150.1
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION: 612-339-0331
TELECHAX: 612-339-3361
                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        LENGTH: 740 amino acids TYPE: amino acid
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Matches 405; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                   CLASSIFICATION: 435
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                                                                                                                   FILING DATE:
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740 amino acids
              TYPE: amino acid
STRANDEDNESS: single
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Job time: 26.1175 secs
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Matches 405; Conservat
                                          linear
   LENGTH: 740 am
TYPE: amino ac;
STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: p
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                                                                                                                       | :::|| | :::|| AGAGTIPDPFGGP--RSPTWLATDLSLRVDPIYERITRRWLEHPEELADEFAKAWYKLI 416
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                                                                                                                                                                                                                               PDPMAAAVDIRETFRRMAMNDVETAALIVGGHTFGKTHGAGPADLVGPEPEAAPLEOMGL
                                                   GWGNPNWQGKASNAVTSGIEGAWTINPTKFDWGYFDLLFGYNWELKKSPAGAHHWEPID-
                                                                                                       383 IKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLT
                                                                                                                                                                                                                                                                  -ASIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: GOACHIL, FTRANIIN R.
APPLICANT: OACHILL, FTRANIIN R.
APPLICANT: OIL, JAmes R.
ITHE OF INVENTION: Detection of Isoniazid Resistant Strains
TITLE OF INVENTION: Of W. Tuberculosis
NUMBER OF SENCENCES: 22
CORRESPONDER ADDRESS:
ADDRESSEE: Whethny, Rassch & Gebhardt, P.A.
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STREET: 119 No. 5922575th Fourth Street, Ste. 203
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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FILING DATE: 07-May-1997
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5922575
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TELEPHONE: 612-305-1226
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TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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CLASSIFICATION:
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                                                                                                                                                                                                                                                    144 GSQRFAPLNSWPDNVSLDKARRLIMPIKKKYGNKISWADIMILAGTVAYESMGLPAYGFS 203
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                                                                                    28 HRAIRER---AMSGKCPVM-HGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNY
                                                                                                                          HPPITETTTGAASNGCPVVGHMKYPVEGGGNQDWWPNRLNLKVLHQNPAVADPMGAAFDY
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  Length 740;
  DB 2;
50.3%; Score 2041.5; DB 2;
ilarity 54.4%; Pred. No. 6.1e-184;
Conservative 92; Mismatches 218;
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sequence 6, Appl. Sequence 6, Appl. Sequence 6, Appl. Sequence 6, Appl. Sequence 1811, Appl. Sequence 1919, Appl. Sequence 11, Appl. Sequence 12, Appl. Sequence 12, Appl. Sequence 12, Appl. Sequence 12, Appl. Sequence 11, Appl. Sequence 2, Appl. Seque

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 6, Application US/0984889 Patent No. US20202010580A1 GENERAL INFORMATION: APPLICANT: DIVERSA CORPORATION

-09-884-889-6

DB ID	10 09-09-884-889-6 10 03-09-884-889-8 10 03-09-884-889-8 11 03-09-870-501-1 10 03-09-734-01-78-5 12 03-00-734-01-78-5 12 03-00-734-01-78-5 15 03-00-75-5-10 14 03-00-75-5-12 15 03-00-5-7-5-7-10 11 03-09-7-7-7-7-10 12 03-00-7-7-7-7-10 12 03-00-7-7-7-7-10 12 03-00-7-7-7-7-10 12 03-00-7-7-7-7-10 12 03-00-7-7-7-7-10 12 03-00-7-7-7-7-10 12 03-00-7-7-7-7-10 12 03-00-7-7-7-7-7-10 12 03-00-7-7-7-7-7-7-10 12 03-00-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-	
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Query Match	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	
Score	2290.5 2290.5 272.5 272.5 234.5 167.5 1123 1120 1135 1155 1155 1155	

Result

Description

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	53; 0; Gaps	KDWWPE        KDWWPE	SHYGGL        GHYGGL
	753;	TGTSN	WPADW       WPADW
	<pre>10; Length 0; Indels</pre>	VMHGGNTS 	LMTDSQEW          LMTDSQEW
	B 10; 0;	MSGKCP               MSGKCP	KKDVHA                 KKDVHA
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Sequence 11, Applil

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95 LKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGTGSQRFAPLNSW 154
                                                                                                                                                                                                                                                                                         PDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEK 214
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Patent No. US20020100081A1

GENERAL INFORMATION:
APPLICANT TAKED.
TITLE OF INVENTION: Temperature Stress and a Trangeneic Plant Exhibiting TITLE OF INVENTION: Temperature Stress and a Trangeneic Plant Exhibiting TITLE OF INVENTION: Temperature Stress and a Trangeneic Plant Exhibiting TITLE OF INVENTION: Themcolearnece
CURRENT FILING THE STRESS OSS OSS CURRENT APPLICATION NUMBER: US/09/870,501

PRIOR APPLICATION NUMBER: 19200-172850

PRIOR APPLICATION NUMBER: 2020-06-09

NUMBER OF SEQ IN NOS: 2
SOUTH NOS: 2
SOUTHWENT PRICE AD00-06-09

NUMBER PRICE TITLE OF THE TEMPER PRICE TH
                                                                                                                                 38 GKCPVMHGG---NTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDFDA
                                                                       Gaps
                                                                       25;
    DB 10; Length 745;
                                                                  92; Mismatches 183; Indels
56.4%; Score 2290.5; DE 59.1%; Pred. No. 6e-207;
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                                                                  433; Conservative
                               Similarity
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Query Match
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Matches 433
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                                       323 IGWGNPNMQGKASNAVTSGIEGAWTINPIKFDMGYF-DLLFGYNWELKKSPAGAHHWEPI 381
                                                                                                                                                                                                                                                    382 DIKKENKPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFWADPEYFKKTFAKAWFKL 441
                                                                                                                                                                                                                                                                                       140 GGGTGSORFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPA 199
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US-09-734-017A-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 WADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 CHGNGNASALAPDPKASDVENQGLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYF- 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 TGSORFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGF 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 HPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQG 322
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                                                                                                                                                                                                                                                                                                                                                                                        33 IMLRLAWHDAGTYDV-NTRTGGANGSIRYEBEYTHGSNAGLKIAIDLLEPIKAKH-PKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 YADLHQLAGVVAVEVTGGPTVEFIPGRRD-----SSVCPREGRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 TMENPLAAVQMGLIYVNPEGVNGHPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGN
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                                                                                                                                                                                                                                                                                   Indels 119;
                                                                                                                                                                                                                          DB 10; Length 291;
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TITLE OF INVENTION: Malze Defense-Inducible Genes and Thair
TITLE OF INVENTION: Malze
FILE REPRENCE: 05718/2398718/2398718/2398718/2001-10-23
CURRENT APPLICATION NUMBER: 05/243,120
PRIOR APPLICATION NUMBER: 00/243,120
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                                                                                                                                                                                                                 6.7%; Score 272.5; DB 10
27.0%; Pred. No. 4.6e-17;
ative 36; Mismatches 96
                                                                                                                          ; ORGANISM: Hordeum vulgare L. Haruna-nijyo
US-09-870-501-1
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                               93; Conservative
                                                                                                                                                                                                                                            Best Local Similarity
Matches 93; Conserv
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US-10-027-559-6
SEQ ID NO 1
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TYPE: PRT
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US-10-027-559-6
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46 GNTSTGTSNKDWWPEGLN--LDILHQQDRKSDPMDPDFNYREEVRKLDFDALKKDVHALM 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 RVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPETMENPLAAV------QMGLIYVNP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 ORFAPLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 -- DHANNEFNLPFGNOOPFLSP---RPNONEORVERENALIVSSFSARILDOMRSKNVTP 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDVEN---QGLGWGNPNMQGKASNAVTSGIEGA---WTTNPTKFDMGYFDLLFGYNWELK 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 -----HFFKGILDLVDKSHAQGFSLQHLRPSYFTISASNQVKYIGSYGT------ 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.0%; Score 123; DB 12; Length 1036; Best Local Similarity 18.3%; Pred. No. 0.044; Metche 139; Conservative 99; Mismatches 274; Indels 248;
    PRIOR FILING DATE: 200-04-04
PRIOR APPLICATION NUBER: US 60/366,327
PRIOR FILING DATE: 2003-03-27
PRIOR FILING DATE: 2004-03-27
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID MOS: 782
SOFTWAR: Patentiat.pl Version 3.0.4 (C) 2001 Syngenta ignory: 10.36
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                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                     US-10-259-165-180
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US-10-205-032-10
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                                                                                                                         APPLICANT: Renz, Andreas
APPLICANT: Renz, Andreas
APPLICANT: Relact, Thomas
APPLICANT: Relact, Thomas
APPLICANT: Relact, Thomas
APPLICANT: Relact, Thomas
APPLICANT: Relact, Andreas
APPLICANT: Preud, Annete
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Reference: BASF-Mast. 331-99-98
TITLE OF INVERTION: Incleosides of amino acids, vitamins, cofactors, nucleotides and
TITLE OF INVERTION NUMBER: 04/20/734,017A
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICANTON NUMBER: 60/2171,100
PRIOR PILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 81
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APPLICATION THE WARD, XUN
APPLICATION THE WARD, XUN
APPLICATION TONGER, BECVEN P.
APPLICATION TONGER, BECVEN PROPERTIES TONGER SILENCING TITLE REPRESENTE TONGER PRINCE PROPERTIES.
TITLE DEPRESENTE: 70040 APPLICATION TONGER FIRST ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING TITLE REPRESENTE: 70040 APPLICATION TONGER TONGER PRINCE PROPERTIES TONGER SILENCING TONGER TONGER
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4.1%; Score 167.5; DB 10; Length 176; Best Local Similarity 29.1%; Pred No. 1.7e-07; Matches 33; Conservative 21; Mismatches 61; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/370,620
Sequence 54, Application US/09734017A
Patent No. US20020142422A1
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Publication No. US20030135888A1
GENERAL INFORMATION:
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US-09-734-017A-54
                                                                         GENERAL INFORMATION:
                                                                                                           APPLICANT: Lerchl,
APPLICANT: Renz, A
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153 -TQALNELPPPFFNATQLVDNFASRNLSLEDMVVL-SGAHTIGVSHCSSFAGINNTGDRL 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 GLPAYGFSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPETMENPLAAVOMGLIYV
                                                                                                                                                                                                                                                                                                                                                                                                                            Outery Match 3.0%; Score 120; DB 14; Length 357; Best Local Similarity 18.8%; Pred. No. 0.016; Matches 152; Indels 128; Matches 152; Indels 128;
Publication No. US20020144307A1
GREBAL INFORMATION: Carl
TILLON TO INVENTION: Carl
TILLE OF INVENTION: Male Defense-Inducible Genes and Their
FILE OF INVENTION: Male Defense-Inducible Genes and Their
FILE SPERRENCE: 2017
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APPLICANT INDA, SAVOSBEIL
APPLICANT INTO ANALY TON
APPLICANT HORIKAMA, TUN
APPLICANT HORIKAMA, TON
APPLICANT SHIBA, TADAYOSHI
APPLICANT SHIBA, TADAYOSHI
APPLICANT SHIBA, TADAYOSHI
APPLICANT SHIBA, TADAYOSHI
ARRAYI ON THE OF INVENTION WOVEL POLYNUCLEOTIDES
THE REPERENCE: 249-232
CURRENT APPLICATION UNBERR: US/10/156/761
CURRENT FILING DATE: 2002-05-29
PRIOR PLILING DATE: 2001-05-30
                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12
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                                                                                                                                                                                                                                                                                                           ) LENGTH: 357

; TYPE: PRT

; ORGANISM: Zea mays

US-10-027-559-12
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;; Pred. No. 0.44;
68; Mismatches 207; Indels 252; Gaps 37;
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APPLICANT: Farmet, Chris
APPLICANT: Tang, Xianabhu
APPLICANT: Tang, Xianabhu
APPLICANT: Stoff, Alfredo
FITLE OF INVENTION GENES AND PROTEINS FOR THE BIOSYNTHESIS OF ROSARAMICIN
FILE REFERENCE: 3016-208
CURRENT PRICATION NUMBER: US/10/205,032
CURRENT FILING DATE: 2002-07-26
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      616 RGGGGDGS--FGRVDVVQPVSWAVMVSLAR----LWMSVGVVPDAVVGHSQGEVAAPV-- 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    668 -VGGVLSVADGARVVALRSRVIGEVLAGGGAMVSVGLPVAVVLDRLAGWGGRLGVAAVNG 726
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                                                                                                                                                                                                                                                                                                                               ; ORGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-10
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.0%;
Best Local Similarity 21.0%;
Matches 140; Conservative 68
   Publication No. US20030113874A1
GENERAL INFORMATION:
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1231 -AAELATELGGLGA-EVTFAACDV------SDRDALGHVIAGIPAEHP 1270
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                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Watch 2:8%; Score 115; DB 15; Length 3613; Dest Local Similarity 2:14; Pered. No. 1.8; Matches 199; Indels 214; Matches 136; Conservative 66; Mismatches 199; Indels 214;
APPLICANT: HATTORI, MASAHIRA
THILE OF INVENTION: WORE POLINUCLEOTIDES
FILE REPRENCE: 244-262
CURRENT PLILAGO HOWBER: USCA).
CURRENT FILLNG DATE: 2002-05-29
PRICR APPLICATION WHOBER: UP 2001-204089
PRICR APPLICATION WHOERS: UP 2001-272697
PRICR APPLICATION WHOERS: UP 2001-272697
NUMBER OF SEQ ID NOS: 120109
SEQ ID NO 1432 NOS: 15109
                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Streptomyces avermitilis
US-10-156-761-10432
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ORGANISM:
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                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                          Query Match

2.9; Score 117.5; DB 15; Length 4881;
Best Local Similarity 20.88; Pred. No. 1.7;
Matches 447; Conservative 72; Mismatches 282; Indels 205;
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                      TYPE: PRT CAGANISM: Streptomyces avermitilis US-10-156-761-8481
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US-10-156-761-10432
                                                                            SEQ ID NO 8483
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Sequence 1, Application US/09793708
publication No. US20030104597A1
GENERAL INFORMATION:
APPLICANT: SETLECT, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.

US-09-793-708-1

Sequence 10432, Application US/10156761 Publication No. US20030119018A1 GENERAL HEOMATION: APPLICANT: ONUM. SATOSHI APPLICANT: TREDA, HARUO

ISHIKAWA, JUN HORIKAWA, HIROSHI SHIBA, TADAYOSHI SAKAKI, YOSHIYUKI

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Page

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APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Mely
APPLICANT: BETLACH, Mely
APPLICANT: BETLACH, Mely
APPLICANT: BETLACH, Mely
APPLICANT: MODALEL, Robert
APPLICANT: CHANNEL, Robert
APPLICANT: CHANNEL, ROBERT
TITLE OF INVENTION: COMBINATIONAL POLYKETIDE LIBRARIES PRODUCED USING A MODULAR
TITLE OF INVENTION: THE SER GENE CLUSTER AS SCAFFOLD
CHRENT APPLICATION NUMBER: US/10/201,365
CHRENT APPLICATION NUMBER: US/10/201,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   950 ILDKVRAQTAQVLGYATGGQIEVDRTFREAGCTSLTGVDLRNRINAAFGVRMAPSMIFDF 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
2.8%; Score 115; DB 12; Length 4551;
Best Local Similarity 21.0%; Pred. No. 2.6; DA Matches 138; Conservative 82; Mismatches 232; Indels 204; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION UNIMERS: US 09/141,908
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMERS: US 09/073,538
PRIOR RILING DATE: 1998-05-06
                                                                                                                              ; Sequence 2, Application US/10201365; Publication No. US20030148469A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Streptomyces venezuelae
US-10-201-365-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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APPLICANT: MCDANIEL, ROBERT APPLICANT: MCDANIEL, ROBERT THE DE POLYKETIDE SYNTHASE TITLE OF WITCHTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                       TILE REFERENCE: 300622002121.

THE REFERENCE: 300622002121.

CURREAT FILIAR DATE: 2001-02-22

PRIOR APPLICATION WHERER: US 09/57,440

PRIOR APPLICATION WHERER: US 09/57,440

PRIOR APPLICATION WHERE: US 09/320,878

PRIOR RELING DATE: 1999-05-27

PRIOR RELING DATE: 1998-08-28

PRIOR RELING DATE: 1998-08-28

PRIOR RELING DATE: 1998-08-08

PRIOR RELING DATE: 1998-05-06

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PRIOR RELING DATE: 1999-05-20

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                             679 NSWKPVGSNAYEIRDR-----KTGAVKWT-----ASRVDLVFGSNSLLRSYAEVYA 724
                                                                                                                                                                                                                                                         APPLICANT: BETLAGH, Marian C.
APPLICANT: BETLAGH, Marian C.
APPLICANT: BETLAGH, Marian C.
APPLICANT: METLAGH, Mary C.
APPLICANT: MEDANIEL, Robert
APPLICANT: MEDANIEL, Robert
APPLICANT: MEDANIEL, ROBERT
APPLICANT: MEDANIEL, ROBERT
FILE REPRENCES: 3006-22002-120
CURRENT APPLICATION NUMBER: US/10/160,539
FRIGH APPLICATION NUMBER: US/09/657,440
FRIGH APPLICATION NUMBER: US/09/057,440
FRIGH SELICATION NUMBER: US/09/057,440
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2.8%; Score 115; DB 12; Length 4551;
Best Local Similarity 21.0%; Fred No. 2.6;
Matches 138; Conservative 82; Mismatches 232; Indels 204
                                                                                                                                                                                      Sequence 1, Application US/10160539
Publication No. US20030162262A1
GENERAL INFORMATION:
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SEQ ID NO 1
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                                                                                                                                  RESULT 14
US-10-160-539-1
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678 1182 2		35;	263	294	337	395	446	497	529	579
D EEML-LDRAQLAGLTGPENTVLLGGMBYLGTRYGGTRHGYFTDCBCQLTRDFFVHLTDMG	SULT 15 -09-661-289-31 -09-661-289 -09-	ch 2:8%; Score 115; DB 10; Length 4613; DS 115; Conservative 82; Mismatches 222; Indels 204; Gaps	A APSDERYGDVNRPETMENPLAAVOMGLIYvNPBGVNGH	PDPLRRHANNDEKTAALTAGG DDARWYLRSKSIAAHLAGGGGGLSLALBEDAULERLAGFDGLSYANNGPTATWYGD DDARWYLRSKSIAAHLAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	:HTVGNCHGNGNASALAPDPKASDVENQGLGNGNPNMQGKASNA	VTSGIEGANTINPIKEDMGYFDLLEGINAELKKSPAGAHMBPIDIKKENKPVDASDP 	SIRHNDIMTDADMAIKVNPTYRAICERFWADPEYFKKTFAKAHFKLTHRDL 	GPKSRIIGEEVPAEDLIMODEIPAGNTDYCEEVVKGKIAG-SGLSISEWVST I DSRUGGHSOLPYFEARTARGYERHUGEIRALAAGAEPAVOPALIEREAAEPAELINDEOLEV I DSRUGGHSOLPYFEARTARGYERHUGEIRALAAGAEPAVOPALIEREAAEPAELINDEOLEV	AWDSA	
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620 EEML-LDRAQIMGLIGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGOLTNDFFVNLTDMG 678

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Search completed: October 7, 2003, 19:59:24 Job time: 52.759 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 7, 2003, 19:39:02; Search time 29.6575 Seconds (Withbot alignments) 2441.707 Million cell updates/sec Run on:

US-09-884-889-6 4058

1 MNNASADDLHSSLQQRCRAF......RDFVAAWTKVMNADRFDVAS 753 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters: 283308 seqs, 96168682 residues

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\* Database

Pred. Wo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	catalase/peroxidas	catalase [imported	catalase (AB033631	catalase (EC 1.11.	(BC 1	catalase BH0906 [1	catalase (EC 1.11.	(BC 1	catalase (EC 1.11.	~	catalase/peroxidas	catalase (EC 1.11.	catalase (EC 1.11.	catalase/peroxidas	hydroperoxidase HP	catalase, hydroper	catalase (EC 1.11.	catalase (hydroper	catalase (EC 1.11.	1.1	1.1	_	catalase (EC 1.11.	catalase (EC 1.11.	catalase (EC 1.11.				
CHINATION	QI .	B82186	AF3127	C98160	875113	S71130	B83763	JS0520	T43873	T43874	T43878	T43880	T43881	T43877	T43882	F82584	F95422	T45091	A87626	G91237	C86085	CSECHP	AI0936	A47685	CSEBHT	A40662	T44846	T44562	AC0403	A69529
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	Query Match	71.9	5.5	5.5	6.8	67.3	62.0	1.3	61.3	61.3	1.3	1.3	1.3	1.3	61.3	. 2	55.6	54.4	3.3	1.7	1.7	9.1	1.3	50.9	9.0	ċ	9.5		7.4	6.9
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T00313	533327	T45480	T12282	S71331	T10190	T03595	T10189	S68465	S43157	C96804	S49914	D86214	220866	T09125	T04707
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736	576	494	430	421	421	250	249	250	250	426	250	250	263	250	279
46.8	40.5	36.6	7.7	7.3	7.1	6.9	6.9	8.9	8.9	9.9	9.9	9.9	9.9	6.5	4.4
1900	1642.5	1485	312.5	294.5	287	279	278.5	276.5	276	269	268.5	267	267	263	260
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

7	
RESULT	

catalase/peroxidase VC1560 [imported] - Vibrio cholerae (strain N16961 serogroup 01)

C.Species: Vibrio cholorre C.Date: 18 Aug-2000 \*sequence\_revision 20-Aug-2000 \*text\_change 24-Aug-2001 C.Accession: BBLD

R.Heidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. Clardson, D.; Emoleva, M.D.; Yamathavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers I., R.R.; Mekalanos, J.J.; Penter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A.J.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A.Reference number: A82035, MOID: 20460833; PMID: 10952301

Alacession: BB2186
Alacession: B

A.Map position: 1
C.Kapperfaulty: catalase HPI
E.Kapperfaulty: catalase HPI
E.Mapperfaulty: catalase HP

ö Gaps ö Length 724; Onery Match 71.9%; Score 2919; DB 2; Length 7 Best Local Smilarity 74.1%; Pred. NO. 5.2e-194; Matches 530; Conservative 75; Mismatches 110; Indels

96	89	156	000
37 SGKCPVMHGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPWDPDFNYREEVRKLDFDALK 96	9 SGQCPVMHGGLISASASNANMDWWPKALNLDILHQHDSKTNPLGADFNYREELKKLDVEALK 68	97 KDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGTGSQRFAPLNSWPD 156	OCT THE TAXABLE TO STATE TO ST
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216 276 157 NVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDI 217 YWGDEKEWLAPSDERYGDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPLRTAQQVLET ò g à

248 277 FARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQGLGWGNPNMQGKASN 336 189 YWGSEKEWLAKSGGENSRYSGQRDLENPLAAVMWGLIYVNPEGVDGNPDPLKTAQDMRVT g à g

337 AVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHHWEPIDIKKENKPVDASDPS 396

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		277 FARMANDERTAALTAGGHTVGKUGENGNASALADPPRASDVENGGLGMGNPRAGCKASN 336
13127 110.1228 110.1228 110.1228 12.123 12.1	retium tume iaciens retision 1 iaul, R.; M C.; Guenth C.; Guenth C.; Guenth C.; Guenth G.; Guenth G.; Guenth G.; Guenth G.; G.; Guenth G.; PIDN:AA	Gy 697 GAVEATENDLYFGSNELLEAYSTARYAGONEREKTORAWATKNANDERDY 731  11 ::::
Oquery Mat Best Loca Matches Matches 1	Pack   March   March	Score 2820; DB 2; Length 731; Pred, No. 3.76-187; Indela 0; Gaps G. Higmatches 121; Indela 0; Gaps G. Higmatches 121; Indela 0; Gaps HWANDILHQODNESDHONPENTREUKRIDFOLK HWANDILLDHONDININGTSPHTENKILDFOLK HYDGILHIRHAMHSACTYRIAGSGGGTGSGROUNGPREDISHP KISHADLAILVATHAGTVATESHCENTONGGROUNGPREDISHP KISHADLAILVATESHCENTONGGROUNGPREDESHP HIJHIH HIJ
		Db 196 YWGDEKEWLAPSDGRYGDVSKPETLENPLAAVQWGLIYVNPEGVNGKSDPLATAAQWRET 255

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us-09-884-889-6.rpr

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integrate (RC 1.111.16) - Synethococcus sp. (strain PCC 7942)

Willtenate names and contradase (EC 1.111.17)

Willtenate names processes (2.111.11.17)

Willtenate processes (2.111.11.17)

Willtenate (2.111.17)

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                                                                                                          FSFGRVDIWEPEKDIYWGDEKEWLAPSDERYGDVNKPETMENPLAAVQMGLIYVNPEGVN
                                                                                                                                                                                                                    GHPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQ
                                                                                                                                                                                                                                                                         GHPDPLCTAQDVRTTFARMAMNDEETVALTAGGHTVGKCHGNSKAELIGPEPEGADVVEO
                                                                                                                                                                                                                                                                                                                                  GLGWGNPNMQGKASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHHWEPI
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A; Residues: 2-7;9-15 <MUI2>
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to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasudi
DNA Res 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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Circymords: heme; incominatalloprotein; oxidoreductase
Circymords: heme; incominatalloprotein; oxidoreductase
Fili3/Active site: His (distal axial ligand) #status predicted
Fili3/Active site: Trp (tryptophy: radical intermediate) #status predicted
Fili3/Active site: Trp (tryptophy: radical intermediate) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C;Accession: 875113
                      VPAEDLIWQDPIPAGNTDYCEEVVKQKIAQSGLSISEMVSTAWDSARTYRGSDMRGGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQGLGWGNPNMQGKASN
                                                                                                          AVTSGIEGAWTTNPTKFDMGYFDLLFGYNWELKKSPAGAHHWEPIDIKKENKPVDASDPS
                                                                                                                                                                                                                    IRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catalase (EC 1.11.1.6) HPI - Synechocystis sp. (strain PCC 6803) N;Alternate names: protein s111987
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69.8%; Pred. No. 2.1e-185;
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F;313/Active site: Trp (tryptophyl radical intermediate) #status predicted
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A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04625.1; GSPDB:G
A:Experimental source: strain C-125
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NAIternate names: catalase-percoxidase; hydroperoxidase I
N.Cohtains: percoxidase (EC 1.11.1.7)
C.Specias: Bacillus stearothermophilus
C.Dete: 30-58p-1991 stearothermophilus
C.C.Paccasion: JSG520; A33955c—revision 08-Nov-1996 #text_change 03-Mar-2000
C.Accasion: JSG520; A33955c—xivision 08-Nov-1996 #text_change o3-Mar-2000
                                                                                                                                                                                                                                                                                                                                        94 ALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGTGSQRFAPLNS 153
                                                                                                                                                                                                                                                                                                                                                                       KDIYWGDEKEWLAPSDERY-GDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPLRTAQQ
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                                                                                                                                                                                                                                                                                             TGKCPFHHGATTSPKSSGTTNNDWWPNALNLNLLRQHDKKSNPMGEEFDYAEEFSKLDYD
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                                                                                                                                                   Length
                                                                                                                                         Query Match 62.0%; Score 2514; DB 2; I Best Local Similarity 64.1%; Pred. No. 5.8e-166; Matches 464; Conservative 90; Mismatches 156;
                                                                      A; Gene: BH0906
C; Superfamily: catalase HPI
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C;Date: 0.10ec-3000 | Sequence_revision 01-Dec-2000 | text_change 15-Jun-2001
C;Accession: B83763 | Sequence_revision 01-Dec-2000 | text_change 15-Jun-2001
C;Accession: B83763 | Sequence_revision | Sequence_revision
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                                                                                          Indels
                                        ; Score 2731; DB 2;
; Pred. No. 5.3e-181;
83; Mismatches 125;
                                                                   69.88;
                                                               Best Local Similarity 69.89
Matches 504; Conservative
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A;Molecule type: DNA
A;Residues: 1-735 <STO>
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C: Accession: T4.373 T. Miyal, K.; Trakhinaleaamsai, S.; Yomo, T.; Shima, Y.; Miki, S.; Yamam
Mar, Biotechnol. 17, Se-Gi, 1918
A: Title: Broultionary molecular engineering by random elongation mutagenesis.
A: Reference number: T4371 Z22644; MUID:99116998; PMID:9920270
A: A: Residues: Translated from GB/ZMBL/DDBJ
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Alfesidues: 1-735 CTRA>
B. (Record S.) Negov. 5. Okada, H.
J. Bacteriol. 171, 4871-4875, 1999
A.fritle: Cloning, nucleotide sequence, and expression in Escherichia coli of the Bacillu A.Reference number: A.Sp. NUID:89359121, PMID:2670897
A.Recession: A33955.
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Matches 468; Conservative
Reference number: JS0520
Accession: JS0520
                                                                            A; Molecule type: DNA
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Db   537 AAVEKAARDAGFDVKVPFFPGRGDATOBOTDVESFAVLEPFADGFRNYQKQEYSVPPEEL 596   G23 LLDRAQLAGLTGPEMTVLLGGARVLGTWGGTKHGVPTDCBQQLTNDFPVNLTDMGNSWK 682   Db   597 LVDRAGLLGLTAPEMTVCGGTKTLANTROLHHGVPTDCBQQLTNDFPVNLLDH	RESULT 9 743812	THE STATEMENT OF THE ST

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A;Residues: 1-751 <MAT>
C;Cross-references: BMBL:AB020099; NID:g4140105; PIDN:BAA37011.1; PID:g4140106
C;Comment: For the wild-type sequence, see PIR:JS0520.
A;Genetics:
A;Gene: cat
C;Reywords: oxidoreductase
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                                                                            89 KLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGSQRF
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                                      388 KPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLG
                                                                                                                                                                            PKSRYIGPEVPAEDLIWODPIPAGNIDYCE---EVVKQKIAQSGLSISEMVSTAWDSARI
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Best Local Similarity 64.2%; Pred. No. 3.2e-164;
Metches 468; Conservative 85; Mismatches 160;
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A.; Hitle: Evolutionary molecular engineering by random elongation mutagenesis.
A.; Mctession: T4380
A.; A.; A.; A.; Mulb. 1931.6998; PMID: 9920270
A.; A.; Molecula type: DNA
A.; Mesidues: 1-751 CAMP.
A.; Mesidues: 1-751 CAMP.
A.; Mesidues: 1-751 CAMP.
A.; Mesidues: 1-751 CAMP.
A.; Mesidues: A.; Milb.; 
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PKSRYIGPEVPAEDLIWODPIPAGNTDYCE---EVVKQKIAQSGLSISEMVSTAWDSART 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catalase (EC 1.11.1.6) [imported] - synthetic
C.Species: synthetic
A: Note: cat gene engineered and expressed in Bacillus stearchermophilus
C.Date: 24-Mar-2000 #sequence_revision 24-Mar-2000 #text_change 23-Mar-2001
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                                      YRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQISAD--TGASIADVIVLAGS
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64.2%; Pred. No. 3.2e-164;
ive 85; Mismatches 160; Indels 16;
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A)Gene: cat
C;Keywords: oxidoreductase
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                                                                                                                                                                                              PKSRYIGPEVPAEDLIWQDPIPAGNTDYCE---EVVKQKIAQSGLSISEMVSTAWDSART 504
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catalase/peroxidase XF2232 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species Xylella fastidiosa
C:Species Xylella fastidiosa
C:Date: 18-Aug-2000 sequence\_terision 20-Aug-2000 #text\_change 24-Aug-2001
A:Accession: PB2584
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nuclectide Sequent R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nuclectide Sequent A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Pitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Pitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A87515; MID:20365717; PMID:10910347
A:Recession: F82584

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A. A. Caragania, A. Caragania,

H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. 145 245 305 439 479 499 539 559 592 619 652 619 710 144 263 323 306 ASALAPDPKASDVENQGLGWGNPNWQGKASNAVTSGIEGAWTTNPTKFDMGYFDLLFGYN 365 383 423 204 'Superfamily: catalase HPI C:Keywords: heme: Iton metalloprotein F:126/Active Site: His (distal axial ligand) #status predicted F:136/Active Site: Trp (tryptophy) redicted axial ligand) #status predicted F:364/Active Site: Trp (tryptophy) radical Intermediate) #status predicted --- GTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYRE 85 25 CPYMRASSPETTSAVKCPFNKTAVEGTHNKDWWPNQLRVDLLHQHSNKSNPLGETFDYAK 84 85 EFQKLDYAALKRDLHALMTDSQDWWPADFGHYGGLFIRMAWHSAGTYRIGDGRGGAGRGQ AAVQMGLIYVNPEGVNGHPDPLRTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGN | : |:|:| ::| ||||| | | ||| : :||||| ||| ||||| ADNVGPEPEAGELEVEWINTRIPTQWSNDFFEHLFGYE 366 WELKKSPAGAHHWEPIDIKKBNKPV--DASDPSIRHNPIMTDADMAIKVNPTYRAICEKF 424 MADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPEVPAEDLIWQDPIPAGNTDYCEE----V 620 DVSSFAPLEPFADGERNYVRGDEVVPSEHLLIDRAQLLTLTAPEMTVLIGGLRVIGANVG EVRKLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGTGS SVYEQISADIGA-----SIADVIVLAGSVGIEKAAKAAGYDVRVPFLKGRGDATAEMT DADSFAPLEPLADGFRNWOKKEYVVKPEEMLLDRAOLMGLIGPEMTVLLGGMRVLGINYG GTKHGVFTDCEGQLTNDFFVNLTDMGNSWKPVGS--NAYEIRDRKTGAVKWTASRVDLVF **ORFAPLINSWPDINYSLDKARRLLWPIKKKYGIKISWADLMILAGTVAYESMGLPAYGFSFG** RVDIWEPEKDIYWGDEKEWLAPSDERYGDVNK--------PETMENPL 180 VKQKIAQSGLSISEMVSTAWDSARTYRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVL 500 INQRISASGLGISQLVSTAWASASTFRGSDKRGGANGGRLCLAPQSQWEVNQPQQLSVVL 560 ETLRRVQTEFNAQAGDKRISLADLIVLAGGVGVEQAAKRAGIVVEVPFVPGRTDALQEQT Gaps 54; Length 781; Indels GSNSLLRSYAEVYAQDDNGEKFVRDFVAAWTKVMNADRFDV 751 GSNALLRALAEFYAAVDAQEKFVRDFVAAWSKVMHLDRFDL Query Match 56.2%; Score 2279; DB 2; Best Local Similarity 56.6%; Pred. No. 1.2-149; Marches 41; Conservative 100; Mismatches 176; CPVMHGGNTST-----M.; Tsuhako, M.H.; Vallada, A.Reference number: A59328 A.Contents: annotation C.Genetics: A; Gene: XF2232 246 324 540 653 740 40 980 -11 PB e A QQ νο . 장 원 ..., :: ... oy g 셤 a 셤 셤 셤 ð õ 셤 õ ö ò 윰 à ò ö ö ò

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; Search time 75.4005 Seconds (without alignments) 2577.085 Million cell updates/sec
                                                                      1 MNNASADDLHSSLQQRCRAF.....RDFVAAWTKVMNADRFDVAS 753
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                    830525 seqs, 258052604 residues
                           OM protein - protein search, using sw model
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830525

Total number of hits satisfying chosen parameters:

Searched:

Sequence:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_bacteria:\*
sp\_fung1:\*
sp\_human:\*
sp\_lnvertebrate:\*

sp\_archea:\* SPTREMBL\_23:\*

Database

sp\_mammal:\* sp\_mhc:\* sp\_organelle:\*

sp\_phage: \*
sp\_plant: \*
sp\_rodent: \*

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*

sp\_rvirus:\* sp\_bacteriap:\*

sp\_archeap:

## RESULT 1

01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last Sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last sannotation update)
Catalase-peroxidase KatB (EC 1.11.1.6) (Peroxidase/catalase). 721 AA. PRELIMINARY; Q92GM4;

Logionella pneumophlia. Bacteria: Proteobacteria: Gammaproteobacteria; Legionellales; Legionellaceae; Legionella. KCDI\_ZaziD-446; SEQUENCE FROM N.A.

The strainty—752 of the strainty of the strainty of the strainty—752 of the strainty—752 of the strainty—753 of the strainty—7 

Gaps 10; Length 721; Indels Query Match 72.0%; Score 2920; DB 2; Best Local Similarity 73.3%; Pred No. 1.8e-192; Matches 53; Conservative 77; Mismatches 106;

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## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9zqm4 legionella	O9krs6 vibrio chol	Ogress synechococc	Q8d951 vibrio vuln	Q8u714 agrobacteri	Q9r708 agrobacteri	O8e981 shewanella	P73911 synechocyst	055110 synechococc	O9kee6 bacillus ha	Q9s5k5 bacillus st	Q9s5r0 bacillus st	Q9s5n2 bacillus st	Q9s5k7 bacillus st	Q9s5q5 bacillus st	Q9s5n4 bacillus st
SUMMARIES	QI.	Q92GM4	G9KRS6	Q9R6S9	Q8D951	080714	Q9R708	Q8E981	P73911	055110	Q9KEE6	Q9S5K5	Q9S5R0	09S5N2	Q9S5K7	098505	09S5N4
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	Query ore Match Length DB ID	72.0	71.9	70.7	70.3	69.5	69.4	69.1	689	67.3	62.0	61.3	61.3	61.3	61.3	61.3	61.3
	Score	2920	2919	2870	2854	2820	2817	2802.5	2795	2731	2514	2489	2489	2489	2489	2489	2489
	Result No.	П	7	e	₹	5	9	7	80	6	10	11	12	13	14	15	16

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Gaps

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Length 724; Indels 96 69 156

308 386 456 428 516 488

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Ermolaeva M.D., Vamathevan J., Bass S., Oln H., Dragol I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Mierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            KDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGGGGRAPLNSWPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                   C53E123D12F6DB51 CRC64;
                                                                                                                                                                                                                                                                                                                                                 Ouery Match 71.9%; Score 2919; DB 16; Best Local Similarity 74.1%; pred. No. 2.1e-192; Mecthes 530; Conservative 75; Mismatches 110;
                                                                                                                                                                                     InterPro; IPR000763; Bac_ctase/prase
                                                                                                                                                                                                                                                    TIGRRAMS; TICKRO198; Cat_per_HPI; 1.
PROSITE: PSO0436; PEROXIDASE_2; 1.
Peroxidase: Complete proteome.
SEQUENCE 724 AA; 80650 MM; C53E1
                                                                                                                                                                                                       Interpro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
                                                                                                            Nature 406:477-483(2000).
EMBL; AE004233; AAF94714.1;
HSSP; P00431; IBEK.
TIGR; VC1560; -
                                                                                             cholerae.
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KDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGTGSQRFAPLNSWPD 156
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571 AAGYDVRVPFLKGRGDATAEMTDADSPAPLEPLADGFRNWQKKEYVVKPEEMLLDRAQLM
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Choy H.E.;
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Vibrionaceae; Vibrio.
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AE016805; AA011099.1;
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Nucker F., Pescher G. A., Obliger C.,
Nucleotide sequence analysis, overexpression in Escherichia coll and
kinetic characterization of Anacystis nidulans catalase peroxidase.";
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-i- SHILIARIY BELONS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALAES SUBFAMILY.
EMBL: ARI97161; ARF0581.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGRO0198; CRL_DEL.HD!; 1.
PROSITE; PSO0456; PEROXIDASE_2; 1.
HEMPE; H9drOgen percide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 720 AA; 80119 MW; 196F159307008463 CRC64;
                                                      01-MAY-2000 (TrEMBIrel. 13, Latt sequence update)
01-MAY-2000 (TrEMBIrel. 23, Last annotation update)
catalase-peroxidase (EC 1.11.1.6) (Peroxidase/catalase).
Symethococcus ap. (strain PCC 50.1) (Anacystis nidulans).
Bacteria, Cyanobacteria, Chrococcales; Symethococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.9e-189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
              ġ
            720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.7%; Score 2870;
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InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
                                           (TrEMBLrel. 13, Created)
                                                                                                                                                                           STRAIN-PCC 6301;
MEDLINE-20322938; Pubmed-10863004;
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
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                                                                                                                                                                                                                                                                    Biochimie 82:211-219(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             520; Conservative
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                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID-1139;
                                     01-MAY-2000 (
01-MAY-2000 (
01-MAR-2003 (
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MTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWKPVGSNAYEIRDRKT 696
                                                                                                                                                                                                                                                                                                                  37 SGKCPVMHGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDFDALK
                                                                                                                                                                                                                              AGKCPVMHGGNTASGKSVTEWPNALNLDILHQHDTKTNPLGTSFNYREALKTLDVEALK
                                                                                                                                                                                                                                                                               97 KDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGGGGRAPLNSWPD
                                                                                                                                                                                                                                                                                                                                                                                               NVSLDKARRLLWPIKKKYGNKISWADIMILAGTVAYESMGLPAYGFSFGRVDIWEPEKDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 IRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 VPAEDLIWODPIPAGNTDYCEEVVKQKIAQSGLSISEMVSTAWDSARTYRGSDMRGGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARIRLAPQNEWQGNEPERLAKVLSVYEQ1SADTGAS1ADVIVLAGSVG1EKAAKAAGYDV
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Rhizobiaceae; Rhizobium.
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01-MAR-2001 (TrEMBLrel. 23, Last unnotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
       79570 MW; ELAA67F4E2456F20 CRC64;
                                                         69.5%; Score 2820; DB 16; 71.0%; Pred. No. 1.4e-185; 1ve 86; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                723 AA
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Agrobacterium tumefaciens.
                                                                                                                  Conservative
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       731 AA;
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508; Conserv
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**SEQUENCE FRON N.A.*

**REDLINE-21608531; PubMed-11743194; Miller N., Blanchard M., Millar M. Goodder B., Hidnke G., Gattung S., Miller N., Blanchard M., Millar D., Goldman B.S., Cao Y., Askenard M., Millar D., Millar D., Hourello B., Goldman B.S., Cao Y., Askenard M., Millar C., Millager M., Doughty D., Scott C., Epps A., Liu F., A. Houled K., Gordon J., Vaudin M., Lartchauk O., Epp A., Liu F., A. Planagan C., Circell C., Gultar D., Gurson C., Statr S., Statr S., Gurson O., Lown C., Statr S., Statr S., Gurson D., Lown C., Statr S., Andréde D., Gurson D., Lown C., Statr S., Andréde D., Gurson D., Lown C., Statr S., Andréde D., Gurson D., Lown C., Statr S., Reselv, Ro09932, Andréde D., Aur_INIT.

**Reselv, Ro09932, Andréde D., Aur_INIT.*

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m Mass}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiacese; Rhizobium.
NCBL_TAXID-176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PRINTS: PR0045B: PEROXIDAS: 1.
TICREMB: TICRR00198; cat_per_HP1; 1.
PROSTIE; PS0045B: PEROXIDASE_2: 1.
PROSTIE; PS00678; WD_REPERAS_1: 1.
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DVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGGGGQRRAPLNSWPDN 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 ARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQGLGWGNPNMQGKASNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 ARMANDDEETVALTAGGHTVGKCHGNGKAQDLGPEPEGEDVEAQGLGWLNKKGRGVGCDA
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                                                                                                                                                                                                                                    Reidelberg J.F., Faulsen T.T., Nelson K.E., Galdos E.J., Nelson W.C., Reed T.D., Elsen J.A., Sesheatt. R., Ward N., Methe B., Clayfon R.A., Deby T.T., Tapabla A., Scott J., Beanan M., Brinkac L., Daugherty S., Deby R.T., Dodson R.J., Durkha A.S., Meft D.H., Kolonay J.F., Wanatheran J.D., Umayam L.A., Mhite O., Wolf A.M., Wanatheran J., Welman J., Impraim M., Lee K., Berry K., Lee C., Meeller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.Y., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella encidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 GKCPVMHGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDFDALKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 WGDEKEWLAPSDERYGDVNKPETWENPLAAVQMGLIYVNPEGVNGHPDPLRTAQQVLETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRYIGPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.1%; Score 2802.5; DB 16; Length 728; 71.1%; Pred. No. 2.2e-184; Live 81; Mismatches 119; Indels 9;
                                                                                                                        Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peroxidass; Complete protecme.
SEQUENCE 728 AA: 80980 MW; 354F1B25226EF0E2 CRC64;
                         Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                        MEDLINE-22297686; PubMed-12368813;
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                                                                                                                                        Alteromonadaceae; Shewanella
                      01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                    Catalase/peroxidase HPI.
                                                                                                        Shewanella oneidensis.
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                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                      NCBI_TaxID=70863;
                                                                                                                                                                                                        STRAIN-MR-1
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tumorigenesis.",

MOI. MICTORIO.", 35:447-414(2000).

MOI. MOINTIANTE: BELONGS TO THE PEROXIDASE FAMILY: BACTERIAL

BEROXIDASE/CARTANES SUBFAMILY:

BEROXIDASE/CARTANES SUBFAMILY:

BEROXIDASE/CARTANES CACTASE/FORSE.

INCHEPTO: IPROVOTOS: PROCACIASE.

INCHEPTO: IPROVOTOS: PROCACIASE.
                                                                                                                                                                                                                                                                                      Length 723;
                                                                                                                                                                                                                                    Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 723 AA; 78741 MW; AA531987F535B508 CRC64;
                                                                                                                                                                                                                                                                                    69.4%; Score 2817; DB 2; Length 7; 71.0%; Pred. No. 2.2e-185; ive 85; Mismatches 122; Indels
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                                                                                                                                             ATRICTION ANNOWAY THE PROXIDASE 1.
PRINTS; PRO048; PEROXIDASE.
TIGENEMS; IIGRO0198; CAL_DEL_HDI; 1.
PROSITE; PSO046; PEROXIDASE 2; 1.
PROSITE; PSO0678; WD_REPEATS_1; 1.
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les 508; Conservative
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631 GLTGPBMTVLLGGMRVLGTNYGGTRHGVFTDCEGOLINDFFVMLTDWGNSWKPVGSNAYE 690 111	1731 PRELIMINARY: PRT: 754 AA. P73911 PRELIMINARY: PRT: 754 AA. P73912 P97033. P73912 P97033. P73912 P97033. P73912 P97033. P73913 P73913 P97033. P73913 P73	SEQUENCE FROM N.A.   H.   Wureta N.;

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                                                              62 LKQDLQALATDSQDWWPADWGHYGGLMIRLTWHAAGTYRIADGRGGAGTGNQRFAPLNSW 121
                                                                                                  DIYWGDEKEWLAPS---DERY-GDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPLRTA 270
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                  35 AMSGKCPVMHGGNTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDFDA
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  Gaps
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WEDLINE-2021582; PUMDMG-11058132;
TRKAMI H., NAKASONG K., TAKAKI Y., Meno G., Sasaki R., Masul N.,
Fuji P., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
  10;
  Indels
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Last annotation update)
  125;
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  Mismatches
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  83;
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01-OCT-2000 (TTEMBLED. 15,
01-OCT-2002 (TTEMBLED. 22,
  Conservative
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                                                                                                                                                                                                                                                                                                                              568 AAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWQKKEYVVKPEEMLLDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 SGKCPVMHGGNT --- STGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDFD
                                                                                                                                                                                                                                                                                                                                                                                                   66 ALKQDVRDLANDSQDWWPADFGHYGPFFIRMSWHAAGTTRIGDGRGGGGTGNQRFAPLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVDIWEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDIYWGDEKEWLAPSDERY-GDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPLRTAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 VLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQGLGWGNPNWQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 IRETFGRMGMNDEETVALIAGGHTFGKAHGAGNPDHVGPEPEAAPIEAQGLGWQNTYGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KASNAVTSGIEGAWTINPIKFDMGYFDLLFGYNWELKKSPAGAHHWEPIDIKKENKPVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453 IGPEVPAEDLIWQDPIPAGN---TDYCEEVVKQKIAQSGLSISEMVSTAWDSARTYRGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQISA--DTGASIADVIVLAGSVGIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWKPVGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          688 AYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVYAQDDNGEKFVRDFVAAWTKVMNAD
                                                                                                                                                                                                                                                                                                                                                                          ALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGTGSQRFAPLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRY
"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; witcher Acids Res. 78:4317-431(2000).

Which is Acids Res. 78:4317-431(2000).

HISSP: P004311, AAR.
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                               735 AA; 81530 MW; E93B4B5EBFA3A593 CRC64;
                                                                                                                                                                                                                                         62.0%; Score 2514; DB 16;
64.1%; Pred. No. 1.7e-164;
1ve 90; Mismatches 156;
                                                                                InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
                                                                                                             Pfam: PF00141; peroxidase: 1.
TICKFAMS: PRIO0189; cat_per_HPI: 1.
PROSITE; PS000438; PROXIDASE_1: 1.
PROSITE; PS000436; PEROXIDASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                            464; Conservative
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                             Complete proteome. SEQUENCE 735 AA;
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                                                                                                                                                                                                                                                             Local
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Matches
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us-09-884-889-6,rspt

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563 VGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWOKKEYVVKPEEM 622
                                                                                                                 PVGSNATEIRDRRTGAVKWTASRVDLVFGSNSLLRSYAEVTAQDDNGEKFVRDFVAAWTK 742
                                                                                                                               268 RTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQGLGWGN 327
                 LLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWK
                                                                         89 KLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGSQRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 RERAMSGRCPVMHGGNT---STGTSNRDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ONRONAAOCP-FHGSVTNQSSNRTTNKDWWPNOLNLSILHOHDRKTNPHDEEFNYAEEFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 APINSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 IWEPEKDIYWGDEKEWLAPSDERY-GDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPL
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Matsurar T., Miyal K., Tzakulnaleaamsal S., Yomo T., Shima Y., Matsurar T., Miyal K., Urabe I.; "Evolutionary molecular engineering by random elongation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 743 AA; 84078 MW; A2C5422SAA1C5B6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 9.1e-163;
85; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                   01-WAY-2000 (TrEMBLrel. 13, Created)
WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last anotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.3%; Score 2489; DB 2;
                                                                                                                                                                                                                                                                                                                                                           CAT.
Bacillus stearothermophilus.
Bacteria: Firmicutes; Bacillales; Geobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pricen, Prioliti, peroxidase; 1.
PRINTS, PRIOLIS, PEROXIDASE, 1.
IIGREAMS, IIGREONO198, cat_per_HPI; 1.
PROSITE; PSO0435; PEROXIDASE_1: 1.
PROSITE; PSO0436; PEROXIDASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutagenesis.";
Nat. Biotechnol. 17:58-61(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 468; Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                        VMNADRFDV 751
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717 VMNADRFDL 725
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01-MAY-2000 (
01-MAR-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYGKGKGSDIIISGIEGAMTPIPTQWDISYFDMLFGYDWWLIKSPAGAWQWMAVDPDEKD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQISAD--TGASIADVIVLAGS 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 IWEPEKDIYWGDEKEWLAPSDERY-GDVNKPETMENPLAAVOMGLIYVNPEGVNGHPDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 RERAMSGKCPVMHGGNT---STGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYRBEVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 APLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 RTAQQVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENQGLGWGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 KPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                Matsuura T., Miyai K., Trakulnaleaamsai S., Yomo T., Shima Y.,
Miki S., Yamamoto K., Urabe I.;
"Evolutionary molecular engineering by random elongation
                                                                                                                                                                                                                                      Nat. Biotechnol. 17:58-61(1998).

-- CARANTER, CACTIVIT: 2 H(2)0(2) - 0(2) + 2 H(2)0.

-- EMILIARIT: BELONGS TO THE PEROXIDASE FAMILY. BACFERIAL.

PEROXIDASE/CARALASE SUBFAMILY.

EMBL. A030055, BA336977.1;

HSSP; P00411; 1BJ9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 743;
                                                                                                                                                                                                                                                                                                                                                                                                                            Heme, Hydrogen peroxide, Iron; Oxidoreductase, Peroxidase.
SEQUENCE 743 AA; 83874 MW; AD98CE03326DAB6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                   01-MAY-2000 (TrEMBLrel. 13, Created)
MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last ennotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.3%; Score 2489; DB 2;
64.2%; Pred. No. 9.1e-163;
ive 85; Mismatches 160;
                                                                                                                           Bacteria; Firmicutes; Bacillales; Geobacillus
         743 AA.
                                                                                                                                                                                                                                                                                                                       InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0458; PEROXIDASE.
TOGRAMA; TOGRODAS; CAL_POL_HDI; 1.
PROSITE; PSO0435; PEROXIDASE_1; 1.
PROSITE; PSO0436; PEROXIDASE_2; 1.
                                                                                                           Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity 64.2
468; Conservative
           PRELIMINARY;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                       NCBI_TaxID-1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches 46
                         09S5K5;
         09S5K5
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7

Gaps 16;

62

88

236

447

504

562 536

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APLNSWPDNVSLDKARRLLWPIKKKYGNKISWADLMILAGTVAYESMGLPAYGFSFGRVD 208
                                                                                                                           IWEPEKDIYWGDEKEWLAPSDERY-GDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPL 267
                                                                                                                                                                                                               RTAQOVLETFARMAMNDEKTAALTAGGHTVGNCHGNGNASALAPDPKASDVENOGLGWGN 327
                                                                                                                                                                                                                           PNMOCKASNAVTSGIEGAWITINPIKFDMGYFDLLFGYNWELKKSPACAHHWEPIDIKKEN 387
                                                                                                                                                                                                                                                                            SYGKGKGSDIIISGIEGAMIPIPIQWDISYFDMLFGYDWWLIKSPAGAWQWMAVDPDEKD 356
                                                                                                                                                                                                                                                                                                                            563 VGIEKAAKAAGYDVRVPFLKGRGDATAEMTDADSFAPLEPLADGFRNWQKKEYVVRPEEM 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAVEKAARDAGFDVKVPFFPGRGDATQEQTDVESFAVLEPFADGFRNYQKQEYSVPPEEL 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLDRAQLMGLTGPEMTVLLGGMRVLGTNYGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWK 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVGSNAYEIRDRKTGAVKWTASRVDLVFGSNSLLRSYAEVYAQDDNGEKFVRDFVAAWTK 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKSRYIGPEVPAEDLIWQDPIPAGNTDYCE---EVVKQKIAQSGLSISEMVSTAWDSART
                                                                                                                                                                                                                                                                                                                                                                                                               YRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQISAD--TGASIADVIVLAGS
                                                                                                                                                                                                                                                                                                                                                                                                                           RERAMSGKCPVMHGGNT - - - STGTSNKDWWPEGLNLDILHOQDRKSDPMDPDFNYREEVR
                                                               KLDFDALKKDVHALMTDSQEWWPADWGHYGGLMIRMAWHSAGTYRIADGRGGGGGGGGR
                                                                                                                                                                                                                                                                                                               KPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Matchinal Community of N. Yomo T., Shima Matchina T., Willy K., Trakulnaleaamsai S., Yomo T., Shima Matix S., Yamamoto K., Usabe I.; "Evolutionary molecular engineering by random elongation multadenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLE1. 13, Created)
MAY-2000 (TrEMBLE1. 13, Last sequence update)
01-MAR-2003 (TrEMBLE1. 23, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-Peroxidase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutagenes1s.";
Nat. Biotechnol. 17:58-61(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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NCBI_TaxID-1422;
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                                                 AAVEKAARDAGFDVKVPFFPGRGDATQEQTDVESFAVLEPFADGFRNYQKQEYSVPPEEL
             AAARDIRETFRRMGMNDEETVALIAGGHTFGRAHGAGPATHVGPEPEAAPIEAOGLGWIS
                                  KPVDASDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLG
                                                                                                           LAPDAEDPSKKVPTMMMTTDLALRFDPEYEKIARRFHONPEEFAEAFARAWFKLTHRDMG
                                                                                                                                   PKSRYIGPEVPAEDLIWQDPIPAGNTDYCE----EVVKQKIAQSGLSISEMVSTAWDSART
                                                                                                                                                   YRGSDMRGGANGARIRLAPQNEWQGNEPERLAKVLSVYEQISAD--TGASIADVIVLAGS
                                                                                                                                                                                                                                                                                   LLDRAQLMGLTGPEMTVLLGGMRVLGTNTGGTKHGVFTDCEGQLTNDFFVNLTDMGNSWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsuure T., Miyai K., Trakulnaleaamsai S., Yomo T., Shima Y., Miki S., Yamanoto K., Urabe I., Vara
Pyolutionary molecular engineering by random elongation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.
-i- SIMILANTY: BELOKS TO THE PEROXIDASE FAMILY: BACTERIAL
PROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 744 AA; 83946 MW; 34632D2BB5B109BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
61.3%; Score 2489; DB 2;
64.2%; Pred. No. 9.1e-163;
1ve 85; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Geobacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO0198; Cat_per HPI; 1. PROSITE; PS00435; PEROXIDASE_1; 1. PROSITE; PS00436; PEROXIDASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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PRINTS; PR00458; PEROXIDASE.
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Best Local Similarity
Matches 468; Conserv
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01-MAR-2003
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IWEPERDIYWGDEKEWLAPSDERY-GDVNKPETMENPLAAVQMGLIYVNPEGVNGHPDPL 267
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1. Locechnol. 17:59-61(1999).
1- CARACTIC ACTUTYT: 2 (170/0(2) - 0(2) + 2 H(2)0.
1- STHILARITY: BELONGS TO THE PEROXIDASE FAMILY: BACTERIAL BROSEL, AG020115; BAA7027.11.
HSSP: P00431, 1853
                                                                                                                                                               SEQUENCE PROM N.A. Matternar T., William A. W. Trakulnaleaamsal S., Yomo T., Shima Matt S., Yamamoto K., Urabe I.;
"Evolutionary molecular engineering by random elongation mutagenesis.";

    Score 2489; DB 2; Length 745
    Pred. No. 9.1e-163;
    Mismatches 160; Indels

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TOTATHE, PRODIAS, PERCONDABE.

TOTATHE, PRODIAS, PRODIABLE.

PROSITE; PRODIAS, PRODIABLE.

PROSITE; PRODIAS, PRODIABLE.

IRME, PROSITE; PRODIABLE.

IRME, PROSITE; PRODIABLE.

TOTO, ONLORED CONTINUENCE OF PRODIABLE.

TAS AN, BAIJS WH, 9266E0888180272 CRC64;
                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TREMBLrel. 13, Last sequence update)
01-MAK-2003 (TrEMBLrel. 23, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                            Bacteria; Firmicutes; Bacillales; Geobacillus
                  745
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                                                                                                                                                                                                                                                                                                                InterPro; IPR000763; Bac_ctase/prase
InterPro; IPR002016; Peroxidase.
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64.2%;
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                  PRELIMINARY;
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                                                                                                                                                                                                       Length 744;
Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 744 AA; 84000 MW; 35CEED2142D4F6AB CRC64;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                       61.3%; Score 2489; DB 2;
64.2%; Pred. No. 9.1e-163;
                                                                                                                                                                                                                               85; Mismatches 160;
                                                                 InterPro; IPR000763; Bac_ctase/prase
InterPro; IPR002016; Peroxidase
                                                                                            PFCHM. PFC0141; peroxidase: 1.
PRINTS; PR00458; PEROXIDASE: 1
TICRENAS; TICRE0198; cat_per_HPI; 1.
PROSITE; PSC0436; PEROXIDASE_1: 1.
PROSITE; PSC0436; PEROXIDASE_2: 1.
                                                                                                                                                                                                                               Matches 468; Conservative
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Gaps 16;

Length 745;

Search completed: October 7, 2003, 19:45:39 Job time : 81.4005 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
11276.082 Million cell updates/sec 8, 2003, 06:25:58 October

1 atggaaaatcacaaacactc.....accggtttgatctgaaataa 2238 US-09-884-889-7 2238 Perfect score; Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

5777422 Total number of hits satisfying chosen parameters: 2888711 segs, 20454813386 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database

em\_fun:\* gb\_sts:\* gb\_sy:\* gb\_un:\* gb\_vi:\* em\_ba:\* 9b\_ba:\*
9b\_in:\*
9b\_om:\*
9b\_ow:\*
9b\_ov:\*
9b\_ph:\*
9b\_pr:\* em\_in:\*

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em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htg\_mam:\* em\_htg\_vrt:\*

is the number of results predicted by chance to have a Pred. No.

em\_htgo\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Bacillus Xanthomon Bacillus Bacillus AE016872 Pseudomon Y14317 Streptomyce AY040244 Burkholde Streptomy Xanthomon Streptomy Bradyrhiz Rhizobium Nitrosomo AR098264 Sequence AR215252 Sequence AE010762 Methanosa AL646061 Ralstonia AP003010 Mesorhizo AE007314 Sinorhizo Rhizobium Caulobact Bacillus us Description AY040244 AE005947 AJ438039 B AL939106 AE011760 A AF126956 S AP005937 B AF486647 B BX321862 AE001210 AB0200534 AB020065 AB020065 AB020067 AB020067 AB020092 AB020070 AB020072 AB020073 AB020074 AB020076 AB020076 AB020079 AB020079 AB020081 AB020083 AB020083 AB020083 AB020083 AB020083 ALIGNMENTS RLE438039 AL646061 AP003010 AE007314 SRFRPS AY040244 AE005967 AE016872 AF126956 8X321862 AP001510 AP005937 AF486647 AB020234 DB Query Match Length 11320 198050 340857 10578 311963 3289 295250 302150 10677 298900 314100 100.0 100.0 47.1 45.8 7.114 4.004 4.006 2238 1053.2 1024.2 991.8 Score 951.2 912.4 903.2 903 900.2 896.6 890.8 Result è. υo 000

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ORGANISM

Unclassified. 1 (bases 1 to 2238) Pobertson, D.E., Sanyal, I. and Adhikary, R.S. Catalases Unknown

REFERENCE AUTHORS TITLE JOURNAL FEATURES

Patent: US 6074860-A 7 13-JUN-2000; Location/Qualifiers

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KEYHORDS Ralstonia solanac SOURCE Ralstonia solanac ORGANISM Ralstonia solanac Bacteria: Protecol Burkholderiaceae	1 S2	Gen Nat 216 118	REFERENCE 2 (bases 1 to 1: ATTHORS Boucher,C.A. TITLE Direct Submission JOURNAL Submitted (05-DEC	Cremicux, CP5/05, Moleculaire describert, 31326 Cast 19857, 31326 Cast 198587, 5000	118 koute de Nari URGV, 2 rue Gaste Laboratoire de Bi F31326 Castanet	INKA, BPZ Christian http://se	source 1198 /morganis// /mo	ø	CDS 151 84	/note="f Gene nan predicte predicte	/codon_s /evidenc /transl_ /product	SUBULT /Proteil /Ab_xrei	/db_xre /transle APGEPLDA GLQOETAI	KOS* KOS* KOS* Ygene ** / gene ** / note **	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   er@toulouse.inra.fr
.toulouse.inra.fr/R.solanacearum.html
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ype="genomic DNA"
n="GMI1000"
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"synonym: RS05083"
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                                                                                         a; Ralstonia.
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TAPSKGSVOLDDSVKRTHLAATLOTVDNQALYTAASGTA IRGSEPAAFSSGAASTA
PAAPDPQOPYGIANTVKGTV NNAA IRGSGKAGVILLQDBARPY PLQADVTVGKTRID
LAAT INPSSLIALDEALHISGASMAHIY PLIGVYLPDYPPPDYRGRLIGERRQGSS
                                                                                                                   WRYEGPTGRVGGSDJ.GGTLTPAMRPEPGQRPOLJGELVSHQLLFADLAPI IGADSHAS
KORRDAPURQD ENDVILPPEPERTURMIN IDADVETGER IVRTADLPIDHLVHTKLD
DAVILLIDPINGVAGGTLTSHIRLIGGSAPROABALAARHEK IRQLEPMISSHARJ
                                                                                                                                                                                                                                             GEINGDARLSATGNSVAALLGASNGELKTINPGGTVSKTILEAMGLNVGNVILTKLFG
DRQVSIT NAAADGEPVSTSCLAQARTEVOVDQAVINTGATSKRESSIDFTIHPDSKGL
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PGGKLLADVRQRPTAPPPGKVYRSGGTGRAADGSPKDPAAAPARQPALPLRDPTTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="RS05080"
/function="miscellaneous; hypothetical/global homology"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"PROBABLE TRANSMEMBRANE PROTEIN"
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD'
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/note="synonyms: RS05079, RSc0775"
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complement(6890. .8257)
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Pred. No. 2e-265;
0; Mismatches 66
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/transl_table=11
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AYGRPPAINGDALTWRKBOSSGNRAYVEPRELIAGDIAIGHDRAKOGPHVAYURL
FRYLLAHLLHARIAILSWILDPBAIALENDSQNRINRFFFFGAQDSQSSGSPSOMKLELRE
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'Procein 1d-cad144731'
'Ab xref-grid 127783'
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OSTLAGOSAN METERPYSG IGGREDGIVOY LETGSPOTGIODAGPHEEN VORTER SERN 
TERBOYRA LAEYLETVPANSTGRORAFIGNSTPRIVTALKERS TETT IDAALKILKING 
ATCHAOLOGSTPOST FOR PELLAIROKANDOTRILVAN VORHIGIERRAGDRHIGHPAKSRO, 
LEDGALAALLAYTTRGEODAFPALTADETAKRRHOY.
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Complement(1552-1781)

Actor="Syronym" Re05081

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/transl_table=11
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predicted by Homology
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2263. .3552
/gene-"RSc0772"
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/gene="RS05081"
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8 6938 W N N N N N N N N N N N N N N N N N N N	
6998 2190 6938	
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Oy 1590 GGACTTTAACCAGGCGCAATCAGATAACAA	510 AGGANACGTRGCTCTGGAACTTATGGGCTTTAAAACTTTTGGTTTTGCAGGTGGCAGAGC 569
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Qy 1470 CTCTGACAAGCGCGGGGGGTGCCAACGGTGC 	390 CTTCGCGCCTCTCAATAGCTGGCCAATCTGGCAATCTGGCATAAAGCACGCTTGCTT

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., Asamizu,E., Kato,T., Sasamoto,S., A., Kavashima,K., Khute,T., A.M., Matsumoto,M., Matsuno,A., A.M., Shimpo,S., Sugimoto,M., Tas,S., Sugimoto,M.,

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//proden_10=14020363.**
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pmcdisatiopgnalfylightadkvisaikgfggwylktsletredilrealig
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RIPRIAALITILLIVUVIVIVIVIVISSAIWAGGELSORIPTWIGELGAITASSTIABSTIA
RIPRIAALITILLIVUVIVIVIVIVISSAIWAGGERSORIVITETRIVAGGERSORIASSAI
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RITPGAADADADVSORPPLALNEBRGAELVRYPOPETUGYTELLRPGRAKSKEEL
COAPTWRDTYGAELARFIEERAETY AARGLFTERF"
complement (3601. . 5871)
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DDTRSLMPRDVSFISEAIKERGITVIDVVKALAKRGFREEAENLLDVVKLRLSGDYLQ
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FALNYIPFIGPLMATIFPTLFATAQSGSWQLALIVFVGLNVIQFAIGSYLEPFITGAS
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DEARHIRYRNLGPAANGSAKDDVVIGISPAFGLKLYRTTAGHRLSEVLGAMLDAIHAR
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                                                                                                                                                                                  /gene="ml16722"
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/gene="mlr6724"
7907. .8404
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9371. .10375
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RASLEGORGHRYCULAPERBAMGYTVEVRARLAAGWGTSCHAZARLGAFROGRD
RSLGORGHRYCLAFRIADAGGYSCHAZELGARGGETVYTKTTSALTGHILALLHRIG
IRNVICCGIFTDGCVSSTVRSLADESYAVIVLEDCCAAATEDLHRKELEIINMIYCHY
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RAAABIGGIGGEGVOVDTSILASIESALAVAARARKSIDVIJAMGOLFPONKLEDNIS
OMBOVOTNILKGTFHAYKAAVPILKTSNOST VITSSITOR TITGFGGESTRGAFKAG
GLOFFNYT CELAKTOL TIVANNYPELITY VELOLGGEDTO TRAASI PLIKELGTVEDI
GTAATIYFASKERGOVYGOTI TVOGOGILBESILAJA*
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DVALIPGRARNGTFTRNFWGFENDFYRAESRDFKTITGSLLISVIGICATTY
SKCHVARY PTELDWYAKAFSDCWINFELIPVGSFWGGWGTQLMSLLLISSFACGMAFH
NTASKTIV SLARGGVLPQATAETHDHHGFPRKASALGSVLAAVWLLIYGLAYGFDDDS
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LVYTLVANLATLGGTNGFAKSIPYVGLAILIVGLIWGFYLKSANPKAYENIGHWVNEG
                                                                                                                                                                        Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research 110stitute. The First Laboratory for Plant Gene Research; Yana 110stitute. The First Laboratory for Plant Gene Research; Yana (G-mail: Ranschedkazu, Chiba 292-0812, Japan (G-mail: Ranschedkazua or. F).

Teliktp://www.kazusa.or. jp/rhizobse/,
Telis1-438-52-9955(ex. 2338), Fax:81-438-52-3934)
On May II. 2001 this sequence version replaced g1:11994985.
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/proteln_id-"BAB52959.1"
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complement(2477. .3175)
gene="mil6720"
/note="hypothetical protein"
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Direct Submission
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198112 CGGCGCCATACGTTCGGCAAGACCCATGGTGCGGGTGACGC---GAGCCTGGTGGGTGT 198168
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                                                                                                                             810 GGGTGGACACATTCGGAAAAACCCATGGTGCTGCCGATGCGGAGAAATATGTGGGCCG
                                                     TATTCGTGAGACTTTTGGCCGAATGGCAATGAATGACGAAGAAACCGTGGCTCTCATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      870 AGAGCCTGCCGCCGCAGGTATTGAAGAAATGAGCCTGGGGTGGAAAAACACCTACGGCAC
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                                                                                                      630 CAAGCGCTATGAAGGTGACCGAGAGCTCGAAAATCCCCTGGGAGCCGTACAAATGGGACT
                                                                                                                                                                                                   CATCTATGTAAACCCCGAAGGACCCAACGGCAAGCCAGACCCTATCGCTGCTGCGGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGATCCGCCGGTCGGACCAACCGTGATTGGTGGCCGAACCAGCTGAACGTCCAGATCCT
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; Pred. No. 1.2e-256;
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10712. .11839
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EGGA I EDOGLGRKST FGTGVGKDA. TGGPEVTWSOTPTRYSNIFFENLFNHEWELTRS PROAYOWKANKATI PDD TOPS SKINGTRATITUDLEREPDA IVER SIRRILERDDERA DAPARAWK KLITHEDGGPKYRTLGPEVPAEDLI WOOV I PAYDHALVDETDIAGLKAKI. ASGLSVQELVSTAWASASTFRGSDKRGGANGARĪRLAPQKDWEVNRPAQLARVLSVLĒ GIQRDFNAAQTDGKKISLADLIVLAGGAAVĒKAAKAGGHDITVPFTPGRMDASĒAQTD AASFAALEPRACERNY ST'RROGENK PERALUDRAGILTI I APENTY I VYGGIRVIKA GEPKHOYET SRPEALINDET VYULLMATON PEI I EGEBOY YEGIDRRIGAARNT GERYO LITEGSIGLARA PEY AGSDAREK PKID VAANT VANADREDIV

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gene

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//octo="gliumer prediction; similar to TED2, a putative quinnon oxidoreductase, from Zinnia elegans, BAMO6460, and guinno cowpee, TI1672, also similar to putative oxidoreductases from Mycobacterium luberculosis, Agrobacterium tumifaciens, etc. Zinc-bindng family\* /product-\*probable oxidoreductase\*
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LIDEPTNNLDRDGRRAVIGLLSGWRSGALVVSHDRELLEERDAIIELTSLGTKRYGGGW SAYQAARAVELZAAQOSLTLARKTADEVDRKARALAERLDKRDASGTRKAAKGDWPRI LIVORRSKABESSRRSKTSKARRALDANTARAKALBYTADERTSTRLEWELDARG VLAPDGYTAGYDDARTITRDLESELVGPRRYSTGPROSGSGTSLLKVYTGELPPRGT VSWNPPFILLDGSSTLEREFTLENERTRARAGASDINGRAALASPRRADAALQBYE ALGSGGVIRAGLAGGSDPPSLLILDEPTNHLDIDSIEAVERGLISYDGALVVYSH /product-\*probable ABC transporter, ATP-binding protein\* //protein.id-\*ARA5591.1\* /Ab\_xref=GT:4534465\* 9057.

.9713

gene

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SYLEICHYLDDLLEGANNRYRLLSSSPDABSERIRESRANVEYAMPPENRRLOA damidement(1992. .10455)

gond-"SM8289
- Thoresses: Adaptation"

fonce-gonden prediction; very shillor to Ohr, a putative
stress-indiced protein, from Bradyrhizoblum Japonium, /function="Miscellaneous; Unknown" /note="glimmer prediction; putative bacterial regulatory protein, tefR family" /product-"hypothetical protein" /protein\_id-"AAK65948.1" /db\_xref-"GI:14524464" complement(9922. .10455) /codon\_start=1 /transl\_table=11 /gene="SMa2387" 9057. .9713 /gene="SMa2387" /gene="SMa2389

gene

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4946 4886 4826 264 324 145 ATCTTACGCCAACATTCATCGCTATCGGACCCAAACGACCCGGATTTTGACTATGCCGAA 205 GAGTTTAAGAAGCTAGATCTGGCAGCGGTTAAAAAGGACCTGGCAGCGCTAATGACAGAT 4945 GAGTTCAAGAAGCTCGACCTCGATGCGCTGAAGCGGGACCTGCGTGCACTGATGACGGAT TCACAGGACTGGTGGCCAGCAGTTACGGTCATTATGGCCCCTTCTTTATACGCATGGCG 4885 regendencesecceseccactresecaretaresecsecretrearececaresec 325 TGGCACAGGGCACCTACCGTATCGGTGATGGCCGTGGTGGCGGTGGCGGTCCGGCTCA 265 셤 ð a à g g à ð

4706 4825 TGGCACAGCGCTGGCACCTACCGTATCACCGATGGCCGTGGCGGCGCGCGGCCAGGGTCAG 4766 4705 TIGCIGIGGCCGAICAAACAGAAATACGGCAACAGGAITICCIGGGCGGAICIATIGAIT 4646 444 504 385 CAGCGCTTCGCGCCTCTCAATAGCTGGCCAGACAATGCCAATCTGGATAAAGCACGCTTG 4765 CAGCGTTTCGCGCCCCCTCAATAGCTGGCCGGACAACGCCCAATCTCGACAAGGCCCGACGT g à g ð 셤

4586 505 CTCACAGGAAACGTAGCTCTGGAAACTATGGGCTTTAAAAACTTTTGGCAGGTGGC 4645 CTGACCGGCAATGTCGCGCTCGAATCCATGGGCTTCAAGACCTTCGGTTTTGCCGGGGGC 565 AGAGCAGATGTATGGGAGCCTGAAGAAGATGTATACTGGGGAGCAGAAACCGAATGGCTG ŏ g à 윱

564

4529 625 GGAGACAAGCGCTATGAAGGTGACCGAGAGCTCGAAAATCCCCTGGGAGCCGTACAAATG ă 셤 4468 GGTCTCATCTATGTTAACCCGGAAGGCCCGAACGGCAACCCCGGACCCGGTTGCTGCTGCCGCG 4409 셤

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                                                                                                                                                                                                                                                                                                                                                                                    ESSLGSGVMMSPEGY ILTNNHVTTGADQIVVALKDGRETIARVIGNDPETDLAVLKID
                                                                                                                                                                                                                                                                                                                                                                                                                                   LKNLPATITARSDGIRIGDVALAIGNPGVGCTVTWGIISATGRNQJGLANTEDPIOT
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TEVWYPPREETEINTLAALAACHSPRYTTEAGANALALASTESPKKORVGP
GNIYVATAKHYTGOVGIDNAIAGPSELLVVOOGTDDPAIANDLEGGAENDRAGAT
VSPDAREELDKVAASTULLPPMARATPTSTSINGMACHIXVNDAGATSVARTAPEH
LELSVANDEAMALHITHAALPHTSEALGOPGACHWITAPSGSTAFSSPLGVYP
POKRESIIVGSPEGASELGKYASVLAAGESLSGGIARSAETATDLDAKTGBLEEGKY
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/protein_id="asa658887.1"
/db_xref="G1:2884888888" /
/translation="MTPTAIRRLDAADPDFARHLDHLLSWESVSDDSVNQRVLDIIK
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Complement(5712...6164)

Anotes Inilar to (8715979604; identified by sequence similarity; putative*
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/locus_identified by match to TIGR protein family HMM
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//ocus_stag="PSPT04438"
//ocus=stainlar to SP:034651; identified by sequence
s/mailarity; putative
                                                                                                                                                  protein"
      sequence similarity; putative"
                                                                                                                                           /product-"trypsin domain
/protein_id-"AAO57884.1"
/db_xref-"GI:28854822"
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complement(9444. .10079)
/gene="hisG"
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/locus_tag="PSPTO4436"
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/gene="hisc"
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complement(6921. .7973)
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/gene="hisD"
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Obrpytyonbywyfhystranuyoklsgyvongehlabganrillddifrorlidalih
Prinahthohadrippptoptptrpkovarkspwypomldbhygikk"
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/product-*sulfate adenylate transferase, subunit 2*
/protein_id-*AD057882.1*
/f.can id-4.0d-*NOXLYHIKGROEAESHIJIREVAREPHEPHYMIYSIGKDSAVKHI
LARKAFERSKIDEPWHYDTHERFOBATEREDWEBHGLIJTH HYDGAYGEINEP
THGSAKHTDIKTIEGLIQALDKHFEDBAYGGARDERSSAKERYTSERSKHRWDR
NOYRELMHYNKGYNKKGEINYPKISHTGATELDHOYITLKGTITUPLIFALSHOVER
NGTLIHIDDREILEHINDERSSITVKKNPRFTLGCTPLTGANPSSANISLYDIQPAL
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DVHPPVGHWYQLARQLDITVBGPLDEBNAVVGLIGSLSEWFARDPARRVODALGRE
PLLIESSGWIRRVGKTGGGGCYTDQAVLGSVDLFLSGRASEQTFHSARRNDISFIAA
BHHATERGVGALGYLARREALEHFIDCNPT"
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/note="similar to GB:231695, and PID:469144; identified by
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//note="gimmlar to GP.11992146, and SP.P21156; identified by sequence similarity; putative"
_codon_start=1
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frote-"similar to SP:050274, GB:233105, and PID:530438;
fouritied by sequence similarity; putalive"
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/locus_tag="pspro4433"
complement(2586, .3503)
/gene="cys0"
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/locus_tag="PSPTO4434"
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/locus_tag="PSPTO4434"
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/gene="cysN/C"
db_xref-"GI:28854818"
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                  similarity; putative'
/codon_statt-1
/codon_statt-1
/product-Arp Dhosphoribosyltransferase'
/product-Arp Dhosphoribosyltransferase'
/db_xref-6T: 28854885'
/db_xref-6T: 28854885'
/frenslaton_on-MutlaisKGRILDFULLARGIVPTENPDKSRKLIPPTQAD
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                                                                                                                    Length 311963;
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                                                                                                                   42.5%; Score 951.2; DB 1; Length 65.6%; Pred. No. 1.1e-245; tve 0; Mismatches 678; Indels
/locus_tag="PSPTO4439"
/note="similar to SP:034520; identified
                                                                                                                   Query Match
Best Local Similarity 65.6
Matches 1471; Conservative
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Best Local Similarity 65.9%; Pred: No. 1.2e-240;
Matches 1404; Conservative 0; Mismatches 716;
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GVERDWGHISIQAVTEALHALTAAGLVERTEERGHFARYARYARYGWGHHHIVGRSGGAN
ADVDCAVGDAFGLTAAGLVERTEERGHFARYGRSFS*
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(bases 1 to 2904)
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Related entry: Y14356.

Cocation/Oubmitters

1. 2960/Qualifices

1. 2960/Qualifices

Angewandterserver and the property of Strain-Turks, described by H.Zahner, University of Strain-Turks, described by H.Zahner, University of
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1143 GAGGGGAGGAGGACTTACTGGGGTCCCGAGACCTGGCTGG	ACCTTCGGAAAACCCATGGTGCTGCTGCTGCTGGAGAAATATTGTGGGCCGGAGAGCTGCCCCCCCC	1180   GAPTAGGARANATTCCCCGGGGTCTCTARANAGCCTGAGTGGGTTCCAGAGGGTTCC   1239   1191   11   11   11   11   11   11
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2630 CGGGCGCAGCTTCTGTCGCTTTCGGCACCAGAATGACTGCTTTGGTAGGC 1899 STACTGGGCACCAACTACGACGGTTCGCAGCATGGAGTGTTTACAAATAAG 1959 CTATCCAATGACTTCTTTGTAAACCTGCTAGACCTCAACACTAAATGGCGA 2019 SAATCAGACAAAGTTTTTGAAGGCAGAGACTTCAAAACTGGCGAAGTAAAG 2079 ACCCGGGTAGACCTGATCTTCGGATCCAATTCCGAGCTAAGAGCCCTCGCA 2139 SGCTGTGCAGATTCTGAAGAAAGTTTGTTAAAGATTTTGTGAAGGCCTGG 2199 GCCAGCGACGACGACGAGGAGAGTTCGTCAAGGACTTCGTCGCCGCGTGG 2750 linear BCT 03-OCT-2002 07-JUN-2002) Lab. of Biotechnology, Chulabhorn Research Vipevadee, Bangkok 10210, Thalland date by submitter ission 04-SEP-2002) Lab. of Biotechnology, Chulabhorn Research Vipavadee, Bangkok 10210, Thalland 4910 bp DNA linear BCT 03-0CT-200 ta pseudomalle! ATP-dependent DNA hellcase protein Recs partial des, and oxidative stress regulatory protein , catalase-peroxidase protein KatG (katG), and DpsA is, complete cds. Research .. Sallabhan, R., Whangsuk, W. and Mongkolsuk, S. Gerla pseudomaltel oxyR gene: expression analysis and acterization control of 2002)

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WNYTCPMPNTLHAMEEQYNELMLAVDLVAERIRTLGVVAEGTYREPAKLSSIPEADG VPAAEEMIRQLVEGHEAVVRTARAIFPDADAASDEPTADLLTGRLGTHEKTAMHLRSL LA* B34 a 1590 c 1736 g 750 t ORIGIN	Guery Match 41.6%; Score 932; DB 1; Length 4910; Bef Local Similarity 65.8%; Pred No. 11.52-240; Matches 1428; Conservative 0; Mismatches 713; Indels 27; Gaps 4;	9y 77 CGCTTAAGCAAGTGGGGGCACCAAAAACGGGATTGGTGGCCCAACATGCTC 136 12 1786 CGTTCAAGCCCAACGAAGGCAAGGAAGGAAGAAGGAAGGA	09   137 ACCTGGGGATCTTAGGGGAACATGATGGGAGGGAAAGGAGGGGGAATTGACT 196	Oy 197 ATGCCGAAGAGTTAAGAAGCTAGATCTGGCACGGTTAAAAAGGACCTGGCAGCAGTAA 256  1906 ACGCCAGCGTTCGAAGATCAGACTGAACCTGCGGTGAAGCGCACCTCCACGGCTTCAAGACTGAACCTCGAACCTCCAACGCGTTCAAACACCACCACCACCACCACCACCACCACCACCACC	OY 257 TGACAGATTCACGAGGACTGGTCGACCAGAGATACGGTCATTATGGCCCCTTCTTTATAC 316  Db 156 TGATCACGAGGATTGGTGGCGGCCGGTCGATTTCGCCAAACGAGGCGTTTCATCAACC 2025	317 GCATGGCGTGGCACACGCGCGGCACCTACCGTATCGGTGATGGCCGTGGCGGGGCGTGCT 	Qy 377 CCGGCTCACAGGCTTCGCGCCTCTCANTAGCTGGCCAATCTGGATAAAG 436	9y 437 CAGGCTTGCTTGGCCCATCAAAAATACGGTCGAAAATCTCCTGGGCGGGTC 496 2146 CCGCCCGTGTGTTGTTTGGCCATCAACAACAACGGCGGCGCGCGGGGCGGGC	QY 497 TAATGATACTCACAGAAACGTGCGGGAACTATGGGCTTTAAAACTTTTGGTTTTG 556	9y 557 CAGGTGGCAGAGCAGATGTATGGGAGCCTGAAGAAGATGTATACTGGGGAGCAGAAAACG 616  Db 2266 GGGGGGCGCGCGGAAAAAG 2322	617 ANTGGCTGGGAGACAAGGGCTATGAAGGTGACGGAAGTCGAAA 661  2323 TCTGGCTGAAATGAGGGGGGGGGGAACGGTATTGGGAACGGACGAACGGAACGGCAACGGCGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGGCAACGAACAAAAAA	99 662 ATCCCTGGGAGCCGTACAAATGGGACTCATCTATGTAAACCCGGAAGGACCCAAGGGCA 721  2383 ACCGCGTGCACACTGCAAATGGGCTCTATGTAAACCGGAAGGCCGGAAGGAA	99 722 AGCCAGACCCTATCGCTGCGCGTGATATTCGTGAGACTTTGGCGGAATGGCAATGA 781  2443 ATCCCCAACGTGCGCGCGCGCGCGCAATGGCGACATGGCGAATGGCAATGAATG	9y 782 ATGACGAAGAAACCGTGGCTCTCATAGCGGGTGGACACCTTGGGAAAAACCCATGGTG 841  1	9y 842 CTGCCGATGCGGAGAAATGTGGGCCGAGAGCCTGCCGCGGGGGTATGAAGAATGA 901  Db 2563 GGGGCCGGTGAACGTGGGCGCGAAGCCGGAGGCGCGGGGAACGCAAGCGGAG 2619	Oy 902 GCCTGGGGTGGAAAAACACCTACGGCACGCGGAGAACGGTGGATGACCATGGGCG 961  bb 2620 GCCTGGGGAAAAAGGACGAACGACGAAAAGGGCAAACGCAAACAAC	
REMARK Sequence update by submitter COMMENT On Sep 4, 2002 this sequence version replaced gi:22657796. Location/Qualifiers 1, 490 and 1sm-"surkholderia pseudomalie!"	gene (Amburgher)		/coom_star_ill /rans_table=1	/ CLAME AL OF THE STATE OF THE	7/gene="oxyk" 319, -1278 7/gene="oxyk" 7/gene="oxyk" 7/gene="oxyk" 7/gene="oxyk"	of transcription factors" /codon_start=1 /transl_table=11 /froduct="oxidative stress regulatory protein OxyR"	/proceil_id="AM/7465.1" /db_arief="Gr_10120120" /translation="MTLPELKYIVAVARERHFGRAAEACFVSQPTLSVAIKKLEDELN /translation="MTLPELKYIVAVARERHFGRAAEACFVSQPTLSVAIKKLEDELN /VOIFBRGASSVSYTPVGDQIYTQAQNYLEQTFAIKEIAKOGKDPLIGPFRLGVIYTIG	TO SECURITY OF THE SECURITY OF			RRNRMSNE	CALE PRAMERO SETTING TO AN ACCOUNT TO THE PROPERTY OF THE PROP	TOWERINEP ENLECTSWELTERS POLICY MANIFOLD TO TO THE MEDITAL THE MEDITAL TO THE MEDITAL THE MEDITAL TO THE MEDITA	TO SERVICE TO SERVICE TO THE SERVICE TO SERVICE TO THE SERVICE OF THE SERVICE TO SERVICE TO SERVICE OF THE SERV	gene 4422 ->4910 /dgne-10pa* CDS 4422 -4910	/gue-"non-specific DNA binding protein" /rotes = non-specific DNA binding protein" /rotes = non-specific DNA binding protein" /rotes = non-specific DNA binding protein"	/product="DpsA" /proclact="DpsA" /proclact="DpsA" /proclact="DpsA" /proclact="DpsA" /proclact="DpsA" /proclact="DpsA" /proclact="DpsA" /product="DpsA" /produc

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                                                                                                                                                                                                          to protein family HMM"
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                                                                                                                                                                                                                                                   /product-"sensor histidine kinase, putative"
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/db_xref="GI:13424692"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 912.4; DB 1;
Pred. No. 3.1e-235;
0; Mismatches 711;
                                                                                                                                                                                                          by match
                                                                                                                                        complement(8818. .10587)
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complement(8818. .10587)
                                                                                                                                                                                        /gene="CC3048"
/note="identified
                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
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Best Local Similarity 65.8%;
Matches 1410; Conservative (
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factor RpoD"

/product-"RNA polymerase sigma /protein\_id-"AAK25009.1" /db\_xref-"GI:13424691"

/transl\_table-11

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                                                                        CGGCACCTACCGCATCACCGACGGTCGCGGCGGCGCCGGCCAGGGCCAGCGTTTCGC
                                                                                                             CATCAAACAAAAATACGGTCGAAAAATCTCCTGGGCGGATCTAATGATACTCACAGGAAA
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                                                                 /product='Keicpaalcate hydroxymethyltransferase'
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CINGLENDETREWKRYDELGKRAKSARRRRLVPGGPVATVFRQRSTPFRRRS'
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BLOGELPRRAARVITATROOVALARDILARONDALBLARDROPELFREIGTIP
TLAPVILDATINDIANSPAGIOEVALDENDILARONDALOGOLDALVALVOSPESITE
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DELGGAPD FREETKLILL HERKENLIALITOSOWAPDROFFRGGLF TRAMBISAGTY
ALTDGRGGAGGGGORPAPLINGSERKOLHALITOSOWAPDROFFRGGLF TRAMBISAGTY
ALTDGRGGAGGGGORPAPLINGSERKOLHALITOSOWAPDROFFRGGRET TRAMBISAGTY
AUTGGRGGAGGGGGGRANNAPDROFFRANIANDESTYALLIAGGFFGKRAGAGFFTY
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SPRGARQHQARKABASI PDATADASRHLHTTUSDLAFPDFYER STRHELENBGEF
ADAFABHTKLTHRUNGFYRYLGFEVARDLINGDY TRYDDHEVUDKDI ABLKREV
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AGAPEHGVFI SRPETLINDFFVNILLDMGTQWPVAGKEGFFBGEDRKTGAAKWTGTRV
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                                                                                                                                                                                                                                                                            /gene="oxyR"
/function="hydrogen peroxide sensing transcriptional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="hydrogen peroxide degrading enzyme"
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             biosynthesis'
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larity 65.6%; Pred. No. 9.4e
Conservative 0; Mismatches
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/product-'putative membrane protein'
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/protein_id-'Cha59607.1'
/db_xref-'G1:6137052
/rranb altion-'BRSRARNERSHRARPRGIARRALALGAYTLANGUGTTLANGUGDGGGASARPATARRALALANGUARPATARALANGUARPATARALANGUARPATARALANGUARPATARALANGUARPATARALANGUARPATARALANGUARPATARALANGUARPATARALANGUARPATARALANGUARPATARALANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGUARPATARANGU
Independent N.R., James K.D., Harris, D.E., Ouall, M.A., Kleser, H.,
Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M.,
Conlins, M., Easer, A., Goble, A., Hidalgo, J., Hornsby, T., Howerth, S.,
Hunng, C.H., Kleser, T., Larke, L., Murphy, L., Owell, S.,
Rabbloowiers, R., Sandersen, A., Rutherford, R., Rutter, S.,
Baylor, K., Saurders, D., Shape, S., Squares, R.,
Sanders, D., Shape, S., Squares, R.,
Sanders, M., Sanders, D., Shape, S., Complete, Stratil, B.G.,
Complete, Genome sequence of the model actinomycete Straptomyces
Nature 447 (6895), 141-147 (2002)
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//dece-Scools1 3c. possible histidice kinase protein, len:
44.2 as similar to TR:050497 (EMBL:AL020358) Streptomyces
coelloclot two-component system sensor, 481 and faste
scores: opt: 401 z score: 451.3 E(): 9s-18; 30.24 identity
IN 367 as overlaps contains Pfam matches to entries
PF00512 signal, histidine kinase and PF00672 DUG? Ocean
found in baccerial signal proteins. Contains possible
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//otote="SCF1130; possible membrane protein, len: 292 as;
similar to TR:02804 (PBR:0.1A003447) Streptowyes
coelicolor putative transmembrane protein, 396 as;
scores: opt: 677 z-score: 505.6 E(): 8 6e-21: 43.78
identity in 309 as overlap. Contains possible hydrophobic
membrane spanning region
//canal_cable-1.
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Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces
sequencing team, Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CBIO ISA E-mail: sabésanger.ac.uk
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/protein_id="CaB59608.1"
/db_xref="G1:6137053"
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complement(1031..3359)
/qene="SCO0551"
/note="synonym: SCF11.31c"
complement(1031..2359)
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/note="synonym: SCF11.30"
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/strain-"A3(2)"
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/transl_table=11
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TITLE
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REFERENCE
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                                                                                                                                                                                                                                                                                         CAAGCGCGGCGGTGCCAACGGTGCACGTATACGACTGGCCCCACAAAAAGACTGGGAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Betterla, Actinobacteria; Actinobacterides; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGGCCTGGGCCAAAGTAATGGACCTGGACCGGTTTGATCT 2231
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beta-mannosidase, man. 377 aar, similar to many e.g. MANA_mannosidase, manna endo-1,4 beta mannosidase procursor (E.S. 2.2 manna endo-1,4 beta mannosidase precursor (E.S. 2.2 manna endo-1,4 beta mannosidase cores: 133.7 E): 0, 613.4 identity in 288 aa overlap. Contains w.cemuna 189aal sequence, and pram match to entry PRONJSO estlutase. Callulase (glycosy) Nydrokase (family 5). Also similar to SCZ84.16 (62.28 identity in 288
VADRLGARVVRSSRGLKRASLALGSGDLGVRVEPDGPPELQEAGAAFNTMADRVVDLL
AVERELVADLSHRLRTPLTALYLEADRMGATPSALRVTEAAGQLERELDSI IAAARTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-widelfclemasvlvveddpviraalievljgegravktarger
Ealenforspedvlyvidgledblejdvlaniesistervevlanskedbefeitellan
Ealenforspedvlyvidgespeglemaspevlensderdppstaliges
Eaddynkyrpesgoglaariaalygespeglemaspevlensderdppstaliges
Edlikrefdlataalbansregeriiaevwooppvedotvudyhlsalirregera
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PAGGRAVWFGLQVGVGGVAKAGSSVGSATVTPDGAGGCRTRTVGEGGAAVATVLDTVGRG
GAGSSFEAVCARGAVGTVDPTVRATVAMTAVTLAAVQDGQAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene-'sCO0552.
/note-'sCR1.32.
/note-'sCR1.32.
/note-'sCR1.32.

aa, similar to TR:CA5556 (DMBL:AJ006592) Streptococus
pneumoniae response requiator Rro2, 23 aa; Rasta scores
opt: 583 z-score: 693.9 E(): 2.88-31, 3.34 identity in
237 aa overlap. Contains Pfam matches to entries PF00466
TERNS_TRS_C, transcriptional regulatory protein and
PF00077 response_reg, response regulator receiver domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-'Pfam match to entry PF00486 trans_reg_C, /natanstriblenal regulatory protein, C terminal, score 93.00, E-value 1.7e-36 complement(2710, .3042)
                                                                                                                                                                                                                                                                                                                                        /note-"Pfam match to entry PF00512 signal, Histidine cinase, score 39.60, E-value 7.1e-08"
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/note="SCF73.01c, manA, probable secreted
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/protein_id="CAB59610.1"
/db_xref="G1:6137055"
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/codon_start=1
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/transl_table=11
/product=putative_response_regulator*
/proteat_d="d1"caps5609.1*
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/gene="SCO0554"
/note="Synonyms: manA, SCF11.34c"
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complement(3099. .3536)
                                                                                                                                                                                                                                                                                                                                                                                              kinase, score 39.60, E-v
complement(1712, .1921)
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SCF11.34C, possible sugar bydrolase, partial CDE, len: >278 as: C-tenhus shallar to SW4.DM4_TMETO (DMBL)120093)
Thermomonospora fisca endoglucanase E-4 precursor (EC 3.1.1) (endo-1.4 Peter sylucanase E-4 precursor (EC 3.1.1) (endo-1.4 Peter sylucanase E-4) Cello 800 as; [strat socies] obt. 544 socies 155.0 E(|:1.15e-2] (endit) 1.0 E(|:1.15e-2] 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTDGGGTPGGACSVGYRVVGEWPGGFQGEIAVRNTGSAAIGPWTLAFAFADGOTVTNM
WGGTATQDAGAVSVAPASYTATIPAGGTVTLGFTARKGDTNTAPAAFRLNGAVCATP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 GGCACCAAAAACAGGGATTGGTGGCCCAACATGCTCAACCTCGGCATCTTACGCCAACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.3%; Score 903; DB 1; Length 314100; 65.0%; Pred. No. 1.2e-232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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/gene="SC00554"
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Matches 1386; Conserv
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	12769 ACCGCGAAGCTGAAAACCCCTCGGGGCGTCCAAATGGTTTAATTTGTGTG	820   ACCTTCGGAAAAACCCATGGTGCTGCGGAGAATATGTGGGCCGAGAGCCTGCCCCCGAGAGCTGCCGGAGAGAATATGTGGGCCGAGAGCCTGCCCCCGAGAGCCTGCAGAGACCTGCAGAGACCTGCAGAGACCCAGGCGCGGCGAGGCCGGCGAGGCCGGCGAGGCCGGCGAGGCCGAGGCAGGCTGGAAAACCCTAGGACCGGCAAGGCCTGGAGAGAGCAGCGTGGAAACACCTAGGAACGACGGCTTGGGCTGCGAGGCGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGAGGCCCTTGGAAGAGCCCCAGGGCAAGGGCCTTGGAAGAGCCCCTAGGAAGACCCCAGGGCAAGGGCCTTGGAAGAGCCCTTGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCTAGGAAGAGCCCCTAGGAAGAGCCCCTAGGAAGACCCCCAACCAA	_		1218 CGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

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/product=gluteathlone S-transferase*
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PKPSRALRSGEQLRIDRGGGIFEITVAALSDVRGPAPVAQALYIESDSSREARAQWRO
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/protein_id="AAM36171.1"
/db_kref-"GI:21107456"
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complement(4809, .7079)
/gene="katG"
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4278, 4685
/gene="hslR"
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3416. .4057
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complement(4809. .7079)
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/transl_table=11
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/transl_table=11
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2647. 331.
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/gene="hslR"
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Quagglo R. R. Perrou J. A. Relnach, F. C. Fazah, C. S., Furlan, L. R.,
Canadroo, F. C. Canadrotte G. Canadrou R. G. Cardono J. K.
Chambroo, F. C. Canadrotte G. Canadrou R. B. Cardono J. L. L.
Chambroo, F. C. Canadrotte G. Canadrou R. B. Ferreira, A. J. S.
Ferreira R. C. C. Forto M. II. F. Borney Glack, B. Ferreira, A. J. S.
Ferreira R. C. C. Forto M. II. F. Forney Glack, F. Forneo, M. C.
Trangolo C. C. Gunber A. Ratsuyama, A. M. Kibhi, L. T. Lotte
Jr. Group, F. C. M. Lemons, E. C. M. Lemons, M. P. Locali, E. C. Machadon, M. A.
Hond, C. F. M. Myari, C. Y. Moon, D. H. M. Norelia L. M. Novo, M. T. M.
Okura, V. K. Olivelia M. C. J. Dromo, D. H. M. Norelia L. M. Novo, M. T. M.
Truffild J. Sand, J. A. Sald, S. M. M. Matte, F. F. Setubal, J. C. and
Santos, M. Truffild, T. Tanadro, E. C. Terza, R. I. D. Trindae Gos
Santos, M. Truffild, T. Tanadro, E. W. White, F. F. Setubal, J. C. and
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Josedeu daing Blastx/Glimmer/Genemark*

Josedeu gartt-1

Transl_Leble-1

Pproduct="50s ribosomal protein 119*

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            Kitajima,J.P.
Comparison of the genomes of two )
differing host specificities
Nature 417 (6887), 459-463 (2002)
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	995 CCTGCCAATGGACCAATAACTTTGAAACCTCTTTGGAAGGAGGAGGGAG	1105 CCGGNIGCACATGATCCCAGGAGTCGCAGGTCCATTATGCTCACTAGGGACCTGGCG   1164	1225   TTTGCAGATGCTTTCGCGAAAGCATGGTACAAACTGACACACAGAGATATGGGACCAAAG   1284	GGGFCGATCACTGGTCGATGGAGGAAACCAGGTCGAGGCCGCGGCGCGAGGACCAAACCCTGGTCGATGGAGGCGACGCGCGCG	AGAMACITE ACANGOGGGGGGGGGGGGGGGGGGGTATAGGAGGTATAGGAGGGGCGGAAAAA GGGGGCTGGGACAAGGGGGGGGGG	1555   GAGGGGGTTTAACCAGGGGGGAATCAAAAGAAAGAATCATGGGGGGTGGGCGTGTT 1644
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gene G C DS G G G G G G G G G G G G G G G G G G	CDS Query Matc	Antenes 10 Qy Db 70; Qy Db 70;		0y 3: 0b 67: 0y 35	Oy 4: Ub 66: Oy 5:	Oy 65: Oy 66: Ob 64:

1705 GTGCCTTTCAACCCGGGACGAGCGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTTC 1764

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LITSCVRRRVGHVSLQANYDALHALTAARLVRRIEPPGSPARFEGRVGDNHHHVLGNSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 TCATCGCTATCGGACCCAAACGACCCGGATTTTGACTATGCCGAAGAGTTTAAGAAGCTA
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1884
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Hibh.J.S. and Roe.J.-H.
Direct Submission
Submitted (19-FEB-199) Hicrobiology, Seoul National University,
Kwan-AK Gu, Shin-Lim 9 Dong, San 56-1, Seoul 151-742, Republic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor A3(2)
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Streptomyces coelicolor A3(2)
Streptomycinaen's freptomycetaceae; Streptomyces.
Streptomycinaen's freptomycetaceae; Streptomyces.
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Habhu, J.S., Oh, S.Y. and Ree, J.H.
Regulation of the furk and catc operon, encoding a ferric uptake
regulation of the furk and catc operon, encoding a ferric uptake
regulation of the furk and catc operon, ancoding a ferric uptake
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1.3027
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Oy 1720 GGACGACG Db 2489 GGCCGCG OY 1780 GGGCGCG Db 2549 ACGCCGA OY 1840 CGCCGAA OY 1840 CGCCGAA OY 2690 CTCCTAGA	9y 1900 GGTATGGG 1   1   1   1   1   1   1   1   1   1	APO05937  LOCUES  LOCUES  ACCESSION APO05937  ACCESSION APO05937  REFRANCE  SOURCE  SOURCE  REFRENCE  AUTHORS  RADACTA A.  AUTHORS  RADACTA  RAD
1361 GAGGCGAGGAGGAGGTCTACTGGGGCCCCGAGACCACCTGGCTCGACGACGGCGGCGCTAC	### ACTITICATION OF THE PROPERTY OF THE PROPER	1180   CATTACGACGACCTACTACACACCACCACCACCACCACCACCACCACCAC
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Kaneko, T., Nakamura, Y., Sato, S., Minamisawa, K., Uchiumi, T., Sasamoto, S., Watanabe, A., Idesawa, K., Iriquchi, M., Kawashima, K., Rohara, M., Matsumoto, M., Shimpo, S., Tsuruoka, H., Wada, T., Yamada, M. and Tabkat, S. Complete ganonic sequence of nitrogen-fixing symbiotic bacterium Bradyrhicobium japonicum USDA, 1002)

UNEUD 1239/215.

RENGE ACAMENCAT., Nakamura,Y., Sato,S., Minamisawa,K., Uchiumi,T.,

Rohara,M., Matanabe,A., Idesawa,K., Iriquchi,M., Kawashima,K.,

Rohara,M., Mataumoto,M., Shimpo,S., Tsuruoka,H., Wada,T., Yamada,M.

and Tabhara,M., Matsumoto,M., Shimpo,S., Tsuruoka,H., Wada,T., Yamada,M.

TIE Complete genomic sequence of nitrogen-fixing symbiotic bacterium GRAML DNA Res. 9 (6), 225-226 (2002)

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PRISCI PEPPALISELELIJU VISKI ESPAADSSGGGOV (STRAJGAARISLIN PERKELDTOVAN
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AKHTPEDAWWHILERALPPHINDELEPFVELLASGEROTURAWGWGOWRAGTY
VDDATGERPWAKNAMGLEPTGGROVERAAGODAMRPAPPREMOGRPDARSELGEL
TWENDRASSALETTROPSEDAGAGAAWILARTABLAWGAERLAGGREDAWAAG
GWANGOLIGALEWARGAKTQLINPPPALCTDWGAMILAMGAERLALGHIDWRADOR
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Institute, The First Laboratory for Plant Gene Research; 2-6-7
Kazusa: Kanetari, Kisarzau, Chiba 292-0812, Japan
                                                        (R-mail:kaneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp/rhizobase/,
Tel:81-838-52-935(ex.5338), Fax:81-438-52-3934)
Location/Qualifiers
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Pred. No. 2.5e-229;
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233511 CCAACGCGTGAAATGGACGCACACGCGACGAATTCTAACCCAACTGCACC 233570
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Adhikary RS, Robertson DE, Sanyal I;

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Catalase; epoxidation; hydroxylation; biosensor; paper bleaching;
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/*tag= a
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1..2238
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Microscilla furvescens.
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Mycobacterium tube
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(without alignments)
10499.111 Million cell updates/sec
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core greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                               1 atggaaaatcacaaacactc......accggtttgatctgaaataa 2238
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                 - nucleic search, using sw model
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Maximum DB
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New bacterial catalages, related nucleic acid vectors an
transformed cells - used as oxidising ageing and for de
destroying hydrogen peroxide, e.g. in blosensors
                                                                                                                                                                                           The present sequence is of the Microscilla furvescens or gene. Fragments of the gene can be used to identify rectainee-53ch may be used to catalyse oxidation reactify expeditation or hydroxylation. The enymen can also be us destroy hydrogen peroxida, e.g. in connection with give production, biosensors, contact lens cleaning, pulp/pap pasteurisation of dairy products. Antibodies raised op extains 53ch, om be used to occept libraries for determines.
                                                                                                                                                                                                                                                                                                                                                           purification of cells containing the enzyme.
                                                                                                                                                             Claim 3; Fig 2; 35pp; English
                   WPI; 1998-086953/08
                                      P-PSDB; AAW33810
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Sequence 2238 BP; 634 A; 545 C; 605 G; 454 T; 0 other;

1 ATGGAAAATCACAAACACTCAGGATCTTCTACGTATAACACAAACA 1 ATGGAAAATCACAAACACTCAGGATCTTCTACGTATAACACAAACA CCTTTTACCGGAGGTTCGCTTAAGCAAAGTGCAGGTGGCGGCACCA GACCTGGCAGCGCTAATGACAGATTCACAGGACTGGTGGCCAGCAC GGCCCCTTCTTTATACGCATGGCGTGGCACAGCGCCGGCACCTACC **AATCCCCTGGGAGCCGTACAAATGGGACTCATCTATGTAAACCCCG** Inde CCTTTTACCGGAGGTTCGCTTAAGCAAAGTGCAGGTGGCGGCACC TGGCCCAACATGCTCAACCTCGGCATCTTACGCCAACATTCATCG GACCCGGATTTTGACTATGCCGAAGAGTTTAAGAAGCTAGATCTG GACCTGGCAGCGCTAATGACAGATTCACAGGACTGGTGGCCAGCAC GGCCCCTTCTTTATAGGCATGGCGTGGCACAGGGGCGCGGCACTAC CGTGGTGGCGGTGCGCTCCGCGCTCTCGCGCGCCTCTCAAT GCCAATCTGGATAAAGCACGCTTGCTTCTTTGGCCCATCAAACAA GCCAATCTGGATAAAGCACGCTTGCTTTTGGCCCATCAAACAA ATCTCCTGGGGGATCTAATGATACTCACAGGAAACGTAGCTCTG( **AAAACT**TTTGGTTTTGCAGGTGGCAGAGCAGATGTATGGGAGCCTC TGGGGAGCAGAAACCGAATGGCTGGGAGACAAGCGCTATGAAGGT 19; 8 Score 2238; I Pred. No. 0; 0; Mismatches ö Best Local Similarity 100.0%; Matches 2238; Conservative 0 121 241 61 181 241 301 301 361 361 421 421 481 **4**81 541 541 601 109 199 661 q 셤 셤 g 셤 à ò à ò ò a ò ð g à q à a ò Dp ò g

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tection and	yo 4	196	CTAGAAGGCGCTGGACCAGACCCCTACTCAATGGAGCAATAACTTTTTGAAACCTC 103	1020
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This invention relates to the DNA and protein sequences of a novel to the invention relates to the DNA and protein of the invention of its movel burified cratalsee polypetide. The protein of the invention of its monologue is useful for catalysing the breakdown of hydrogen peroxide. The protein sequence of the invention is useful for modifying amail inflectule. The protein of the invention is also useful for catalysing blochemical reactions, for hydrolysing catalysing blochemical reactions, for hydrolysing protein for inkages and for generating antibodies which bind specifically to the protein. The nucleic acid sequences of the convention is useful as a probe to determine whether a blological sample, such as a soil sample, contains an organism having the nucleic acid or such as a soil sample, contains an organism having the nucleic acid or such in contains an organism having the nucleic acid or such in a probable or purify the protein of redertion of protein of the invention is useful in immunosfinity chromatography procedures to isolate or purify the protein or for detection of protein of the invention is useful in immunosfinity chromatography or invention is heat stable, is heat resistant, and is able to the invention and regain activity after exposure to temperatures of from about 60 to 105 degrees. The present sequence represents the but he sequence requesting the protein of the sequence and regain activity after exposure to temperatures of from should be approached the processing sequence represents the but he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CCTTTTACCGGAGGTTCGCTTAAGCAAAGTGCAGGTGGCGGCACCAAAAACAGGGTTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGGAGCAGAAACCGAATGGCTGGGAGACAAGCGCTATGAAGGTGACCGAGAGGTTCGAA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 TGGCCCAACATGCTCAACCTCGGCATCTTACGCCAACATTCATCGCTATCGGACCCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTTTTACCGGAGGTTCGCTTAAGCAAAGTGCAGGTGGCGGCACCAAAAACAGGGATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GACCTGGCAGCGCTAATGACAGATTCACAGGACTGGTGGCCAGCAGATTACGGTCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCCCTTCTTTATACGCATGCCGTGGCACAGCGCCGCCACCTACCGTATCGGTGATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 CGTGGTGGCGGTGCCTCCGGCTCACAGCGCTTCGCGCCTCTCAATAGCTGGCCAGACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 AAAACTTTTGGTTTTGCAGGTGGCAGAGCAGATGTATGGGAGCCTGAAGAAGATGTATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGAAAATCACAAACCTCCAGGATCTTCTACGTATAACACAAACACTGGCGGAAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GACCCGGATTTTGACTATGCCGAAGAGTTTAAGAAGCTAGATCTGGCAGCGGTTAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCCCTTCTTTATACGCATGGCGTGGCACAGCGCCGCACCTACCGTATCGGTGATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 100.0%; Score 2238; Best Local Similarity 100.0%; Pred. No. 0; Matches 2238; Conservative 0; Mismatches
   antibodies which bind to the polypeptide
                                                    Claim 1; Fig 6; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nvention.
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                                                                                                                                                                                                                                                                                                                                                                                                                      2100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2161 TCTGAAGAAAAGTTTGTTAAAGATTTTGTGAAGGCCTGGGCCAAAGTAATGGACCTGGAC 2220
                                                                                                                                                                                                            GTTTTTGAAGGCAGAGACTTCAAAACTGGCGAAGTAAAGTGGAGTGGCACCCGGGTAGAC 2100
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                                                                                                                                                                                                                                                                                                                                                                                                   CTGATCTTCGGATCCAATTCCGAGCTAAGAGCCCTCGCAGAAGTGTACGGCTGTGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGAAGAAAAGTTTGTTAAAGATTTTGTGAAGGCCTGGGCCAAAGTAATGGACCTGGAC
                                                                                                                                                                                      AACTACGACGGTTCGCAGCATGGAGTGTTTACAAATAAGCCGGGTCAGCTATCCAATGAC
TACATTAAACCGGAGCATAAAGTATCCGCTGAGGAAATGCTCGTAGACCGGGGGCGCAGCTT
                                             1801 TACATTAAACCGGAGCATAAAGTATCCGCTGAGGAAATGCTCGTAGACCGGGCGCAGCTT
                                                                                              CTGTCGCTTTCGGCACCAGAAATGACTGCTTTGGTAGGCGGTATGCGTGTACTGGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene; ss; marine bacteria; catalase; hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding Microscilla catalase protein 53CA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
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97US-0951844.
99US-0412347.
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1681 AAAGATGCTGGCCATGGGGTGCAGGTGCCTTTCAACCCGGGACGGGGGGATGCCACCGGT 1740   1741 GAGCAAACCGATGGAAGCTTTCGAAGCCAGGGGGGTGACGGGTTTAGAAC 1800   1741 GAGCAAACCGATGGGAAGCTTTCGAAGCATAGACCAGGGGTGACGGCTTAGAAC 1800   1741 GAGCAAACCGATGTGGAAGCTTTCGAAGCATGAGCCAGGGGTGACGGCTTAGAAC 1800   1801 TACATTAAACGGAGCATAGAACTATCGGACAGAAATGCACCGAGCGGCAGCTT 1860   1801 TACATTAAACGGAGCATAAAGTATCGCTGAGAAATGCTGTAGACCGGGCGCAGCTT 1860   1801 TACATTAAACGGAACAAAATGACTGTTGGTAGGCGGTATGCTGAGCCGGCGCAGCTT 1860   1801 CTGTCGCTTTCGGCACCAGAAATGACTGTTTGGTAGGCGGTATGCGTAACCGGGCCCC 1920   1801 CTGTCGCTTTCGGCACCAGAAATGACTGTTTGGTAGGCGGTATGCGTAACGGGGCCC 1930   1801 CTGTCGCTTTCGGAACAAAATGACTGTTTGGTAGGCGGGAATGCGTTATGGTAGCCGGGTATTGGTAGCCGGGTATGCGTAACGGGCGCC 1930   1901 AACTACGACGAACAAAATGACTGTTTACAAATAAACCGGGGTATGCGTATCGGACCTAACGGCGCCTAATGCCTTACAAAATGACCGGGGTATGCGTATCGGAACTAACCAAAAATGACCGGGGTATGCGTAACGGGGCTATGCGAATGACTAACAAAAATGAACAAAAATAAACCGGGGTATGCGTAATGACCAGGATACCAAAAATGACCGGGGTATGCAAAAATGACCGGGTATAACAAAAAAAA	1921 1981 1981 2041	2101 CTGATCTTCGGATCCAATT 2101 CTGATCTTCGGATCCAATT 2161 TCTGAAGAAAGTTGTTA 2161 TCTGAAGAAAGTTGTTA 2161 TCTGAAGAAAAGTTGTTA	dy 2221 CodffforctChantan 2238  Db 2222 CodffforctChantan 2238  ART90400 standard; DNA; 2331 BP.	AT90400; The state of the state	isoniazio resi RFLP; kato gene isonicotinic a tuberculostatio Mycobacterium t Key	CDS mutatlon	mutation 1013 /*tag- /note mutation 1079
	### ### ##############################	1021 TTTGGTTACGAGGGGGGCTTACCAAAAGTCCAGGTGAACGTTATCAGTGGAAACGAAAA 1080	1141   TTTATGCTCCCTAGGCCTGGCCTGGTGGCATGGCCTGATTACGAAAAATTTCTCGA 1200	1261   ACACACACANTACCACACACTOCCOCTACCTOCCACCACACACCCCCCCACACACC   1320	1381 GANGGCTTANAGCCTANARYCCTGGANTGGGGACTAGGGTAAGCAGG 1440   1381 GANGGCTTANAGCAAARYCCTGGANAGCAGG 1440   1381 GANGGCTTANAAGCCAAAATYCCTGAAATTGGGATTGAGGATTGAGGATTAGGGTAAGCAGGTAAGAGG 1440   1441 GCATGGCTTCTGCATCTACTATTTAGAAACTCTGACAAGCGGGGGGGG	1501 GGTATACGACTCCACAAAAAAGACTGGGAAGTAAACAACCCTCAGCAACTTGCCAGG 1560	1621 GCAGTATCGTTGGCCGACCTGATTGTGCTGGCCGGCTGCTGCCGGTGTAGAAAAGCTGCA 1680

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       thebroulosis wild-type katc (catalase-peroxidase) gone. Claimed methods of rapidly identifying streams of M. tuberculosis which are resistant to the tuberculostatic drug isoniazid (IMM) are based on the discovery of a mutations in the wild-type gene sequence that confer IMM resistance and which coincidently result in the addition or deletion of restriction admonstrates sizes. Primars (see ANT90401-2) are provided for the PCR amplification of the katc gene ANT90401-6; for use in the restriction fragmant length polymorphism landlysis of the amplification general control and analysis of the amplification fragmant landly polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                Determining susceptibility of Mycobacterium tuberculosis strains to isoniazid - by detecting mutation(s) in the catalase-peroxide gene,
                                                                                                                            eliminates a Ncil-MspI restriction site"
          A to G transversion at base 1079 alters codon 337 from TAC (Tyr) to TGC (Cys) leading to isoniazid resistance, and eliminates a Rani restriction site*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.7%; Score 844.4; DB 18; Length 2331; 63.0%; Pred. No. 1.8e-253; Live 0; Mismatches 801; Indels 15;
                                                                                        alters
                                                                                      'G to T transversion at base 1457 alter codon 463 from CGG (Arg) to CTG (Leu) leading to isoniazid resistance, and
                                                                                                                                                                                                                                                                                                                                                                                                                                            This DNA sequence comprises a consensus of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2331 BP; 455 A; 734 C; 763 G; 379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     susceptibility to INH of the strain. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 31-36; 38pp; English
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1049 1109 1166 1169 1223 749 989 449 512 509 572 569 632 629 689 689 749 803 808 869 869 926 929 986 CGACCAGTGGGAGCC---CGATGAGGTCTATTGGGGCAAGGAAGCCACCTGGCTCGGGGA TCAATGGAGCAATAACTTTTTTGAAAACCTCTTTGGTTACGAGTGGGAGCTTACCAAAAG 047 GAAATGGGACAACAGTITCCTCGAGATCCTGTACGGCTACGAGGGGGGGCTGACGAGAG TCCAGCTGGAGCTTATCAGTGGAAACCAAAAGACGGTGCCGGGGCTGGCACCATACCGGA 344 ATACCTTGGGCCGCTGGTCCCCAAGCAGACCCTGCTGTGGCAGGATCCGGTCCCTGCGGT AAGCCATCCTCTTGTAGACGAAAACGATATTGAAGGCCTAAAAGCCAAAATCCTGGAATC CAGCGCCGGCACCTACCGTATCGGTGATGCCGTGGTGGCGGGGGCTCCGGCTCACAGCG 573 cescaacrecececresaarcearesecricaasacerresecriceserresecricesecr AGATGTATGGGAGCCTGAAGAAGATGTATACTGGGGAGCAGAAACCGAATGGCTGGGAGA CAAGCGCTATGAAGGTGACCGAGAGCTCGAAAATCCCCTGGGAGCCGTACAAATGGGACT CATCTATGTAAACCCCGAAGGACCCAACGGCAAGCCAGACCCTATCGCTGCTGCGCGTGA 810 CATTCGCGAGACGTTTCGGCGATGGCCATGAACGACGTCGAAACAGCGGCGCTGATCGT GGGTGGACACACACCTTCGGAAAAACCCATGGTGCTGCCGATGCGGAGAAATATGTGGGGCCG CGGACACGGTGCGGATACCATCACCAGTGGACTAGAAGGCGCCTGGACCAAGACCCCTAC TGCACATGATCCCAGCAAGTCGCACGCTCCATTTATGCTCACTACGGACCTGGCGCTGCG CCCGTTCG---GCGGGCCAGGGCGCTCCCCGACGATGCTGGCCACTGACCTCTCGCTGCG AGATGCTTTCGCGAAAGCATGGTACAAACTGACACACAGAGATATGGGACCAAAGGTGCG CTACCTGGGACCAGAAGTGCCTCAGGAAGACCTCATCTGGCAAGACCCTATACCAGATGT 393 GGTGCCGGCACCTACCGCATCCACGACGCCGCGGCGCGCCCGGGGGCGCATGCAGCG 453 GTTCGCGCCGCTTAACAGCTGGCCCGACAACGCCAGCTTGGACAAGGCGCGCCGGCTGCT TTGGCCCATCAAAAAAAATACGGTCGAAAAATCTCCTGGGCGGATCTAATGATACTCAC 510 AGGAAACGTAGCTCTGGAAACTATGGCTTTAAAACTTTTGGTTTTGCAGGTGGCAGAGC TATTCGTGAGACTTTTGGCCGAATGCCAATGAATGACGAAGAAACCGTGGCTCTCATAGC AGAGCCTGCCGCCGCAGGTATTGAAGAAATGAGCCTGGGGGTGGAAAAACACCTACGGCAC CATGGACCCTGATTACGAAAAATTTCTCGACGGTACTATGAAAACCCTGATGAGTTTGC

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The invention realies to a novel method of detecting Mycobacterium tuberculosis. The method comprises amplifying the DNA in the sample sto comprises amplifying the DNA in the sample sto perskide a detecting an analysis and interest amplifying the DNA in the sample sto perskide a detection and analysis and interest and the sample stored to the comprises detection in the sample stored to the sample stored t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of Mycobacterium tuberculosis - by amplifying katd
and detecting specific fragment, and optionally identifying
TNRT-estiscat strains by detecting specific mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.7%; Score 844.4; DB 20; Length Best Local Similarity 63.0%; Pred: No. 1.8e-253; Matches 1390; Conservative 0; Misematches 801; Indels
                         /*tag= a
/gene= "katG"
/product= "catalase peroxide"
/note= "the start codon is not indicated"
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GGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCATCTACTTTTAGAAA 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTTTCAACCCGGGACGAGCGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTTCGA 1766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004 GITCACCGAGGCCTCCGAGTCACTGACCAACGACTTCGTGAACCTGCTCGACATGGG 2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2064 TATCACCTGGGAGCCCTCGCCAGCAGATGACGGGACCTACCAGGGCAAGGATGGC---AG 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCGAAGTAAAGTGGAGTGGCACCCGGGTAGACCTGATCTTCGGATCCAATTCCGAGCT 2126
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                                                                                                                1824 CGTGCTGGAGCCCAAGGCAGATGCTTCCGAAACTACCTCGGAAAGGGCAACCGGTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2181 GCGGGCGCTTGTCGAGGTCTATGGCGCCGATGACGCGCAGCGGAGGTCGTGCAGGACTT
                                        1464 GGGATTGACTGTCTCACAGCTAGTTTCGACCGCATGGGCGGCGGCGCGTCGTCGTTCCGTGG
                                                                                       1470 CTCTGACAAGCGCGGCGGTGCCAACGGTGCACGTATACGACTGGCCCCACAAAAGACTG
                                                                                                                                                                               GGAAGTAAACAACCCTCA---GCAACTTGCCAGGGTACTCAAAACACTAGAAGGTATCCA
                                                                                                                                                                                                                                                                       GGAGGACTTTAACCAGGCGCAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGATTGT
                                                                                                                                                                                                                                                                                                                  GGAGTCATTCAACTCCGCGCGCGCGGGGAACATCAAAGTGTCCTTCGCCGACCTCGTCGT
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    M. tuberculosis catalase peroxide (katG) gene sequence.

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390 CTTCGCCGCCTCTCAATAGCTGGCCAACATCTGGATAAAGCACGCTTGCTT	633 GÀNCCAGTÓGÓAGCCCÁTGAGGTCTÁTTÓGGGCAAGÁAGCACCTÓGCTCGGCAA 689 630 CAAGCGTTACAAGCTGACCAAAATCCCCTGGGAGCGTACAAATCGCACTTÓGCTTACAGCATTACAGCATTACAGAGTGACCGAAAATCCCCTGGGAGCGGTACAAATCGCATTACAGCATTACAGCGTTACAGCGGAAACCCCTGCAGCCGCTGCGGGGGGGTACAATCGCATACAGCATTACAGCATTACAGAAACCCATTACAGCAGTACACCAAACGGCAAACGCAAACGCAAACGCAAACGCCAATCGCTGAACCGTGAACCGAGAGGCCCAAACGCAAACGCAAACGCAAACGCAAACGCAAACGCCAAACGCAAACGCAAACGCAAACGCAAACGCAAACGCAAACGCAAAACGCAAAACGCAAAACACGCAAAACGCAAAAACGCAAAAACGCAAAAAA		1056   PCCAGCTGGAACCTATCAGTGGAAACCAAAAGACGGGGGGGG	1230 AGATGCTTTCCCGAAAGCAGGACACACACACACATATGCGACCAAAGGTGCG   1289

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19935 CGACCAGTGGGAGCC---CGATGAGGTCTATTGGGGCAAGGAAGCCACCTGGCTCGGCGA 39879

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This investion relates to a novel method for identifying essential genes for survival or vitulence of mycobacters he method comprises aligning the genomic sequence of a first mycobacterium species or he method comprises aligning the genomic sequence of a first mycobacterium species on a population of the constraint o
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                                                                                                                                                                                                                                                                                                                                                                                                  Identifying and selecting genes for survival or virulence of wyrobocteria by a comparative genomic analysis of the sequences Myrobocterium tuberculosis and M. leprae -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 4; 874pp; English.
                                           22-FEB-2001; 2001US-270123P
                                                                                                                                  (INSP ) INST PASTEUR
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Sequence 82993 BP; 14881 A; 26628 C; 26719 G; 14765 T; 0 other;

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39759 39699 39642 39582 39345 39285 39105 39045 39462 39402 39225 39165 38925 1049 1289 1349 869 989 809 929 TCCAGCTGGAGCTTATCAGTGGAAACCAAAAGACGGTGCCGGGGGTGCCACCATACCGGA 39401 CCCGTCG---CCGGGCCAGGGCGCTCCCCGACGATGCTGGCCACTGACCTCTCGCTGCG 630 CAAGCGCTATGAAGGTGACCGAGAGCTCGAAAATCCCCTGGGAGCCGTACAAATGGGACT 39878 TGAGCGTTACAGCGGTAAGCGGGATCTGGAGAACCCGCTGGCCGCGGGGCTGCAGATGGGGCT 690 CATCTATGTAAACCCCGAAGGACCCAACGGCAAGCCAGACCCTATCGCTGCTGCGGTGA 39818 GATCTACGTGAACCCGGAGGGCCGAACGGCAACCGGACCCCATGGCCGCGGGGGTCGA TATTCGTGAGACTTTTGGCCGAATGGCAATGAATGACGAAGAAACCGTGGCTCTCATAGC 810 GGGTGGACACACCTTCGGAAAAACCCATGGTGCTGCCGATGCGGAGAAATATGTGGGCCG 870 AGAGCCTGCCGCCGCAGGTATTGAAGAAATGAGCCTGGGGTGGAAAAACACCTACGGCAC CGGACACGCTGCGGATACCATCACCAGTGGACTAGAAGGCGCCTGGACCAAGACCCCTAC TCAATGGAGCAATAACTTTTTGAAAACCTCTTTGGTTACGAGTGGGAGCTTACCAAAAG 39521 GAAATGGGACAACAGTTTCCTCGAGATCCTGTACGGCTACGAGTGGGAGCTGACGAAGAG 39461 CCCTGCTGGCGCTTGGCAATACACCGCCAAGGACGGCGCCGGTGCCGGCACCATCCCGGA 1110 TGCACATGATCCCAGCAAGTCGCACGCTCCATTATGCTCACTACGGACCTGGCGCTGCG 1170 CATGGACCCTGATTACGAAAATTTCTCGACGGTACTATGAAAACCCTGATGAGTTTGC 1230 AGAIGCTITCGCGAAAGCAIGGIACAAACTGACACAGAGAIAIGGGACCAAAGGIGCG 1350 AAGCCATCCTCTTGTAGACGAAAACGATATTGAAGGCCTAAAAGCCAAAATCCTGGAATC 39164 CAGCCACGACCTCGTCGGCGAAGCCGAGATTGCCAGCCTTAAGAGCCAGATCCGGGCATC GGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCATCTACTTTTAGAAA 39104 GGGATTGACTGTCTCCACCTAGTTTCGACCGCATGGGCGGCGCGCGTCGTTCCGTGG 1470 CTCTGACAAGCGCGGCGGTGCCAACGGTGCACGTATACGACTGGCCCCACAAAAGACTG 38984 GGAGGTCAACGACCCGACGGGGATCTGCGCAAGGTCATTCGCACCCTGGAAGAGATCCA GGAGGACTTTAACCAGGCGCAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGATTGT GGAGTCATTCAACTCCGCGGGGGGGGAACATCAAAGTGTCCTTCGCCGACCTCGTCGT GCTGGCCGGCTGTGCGAAAAAGCTGCAAAAGATGCTGGCCATGAGGTGCAGGT 38864 GCTCGGTGGCTGTGCCGCCATAGAGAAAGCAGCAAAAGGCGGCTGGCCACAACATCACGGT CTACCTGGGACCAGAAGTGCCTCAGGAAGACCTCATCTGGCAAGACCCTATACCAGATGT 1530 GGAAGTAAACAACCCTCA---GCAACTTGCCAGGGTACTCAAAACACTAGAAGGTATCCA 750 930 1410 1647 1290 1587 셤 g g g 合 à à à g à ö 요 ò ò ò 셤 ò a ò g ò 셤 ò a ò 셤 ç g à g ö a ö 셤 ò 셤 40176 40116 10475 TACAGAAACCACCACCGGAGCCGCTAGCAACGGCTGTCCCGTCGTGGGTCATATGAAATA 40416 39995 CGCCAACTGCGCGCTGGAATCGATGGGCTTCAAGACGTTCGGGTTCGGCCTTCGGCTTCGGCCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCCTTCGGCTTCGGCCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCCTTCGGC 40056 39996 149 269 449 509 629 83 TACGTATAACACAAACACTGGCGGAAAATGCCCTTTTACCGGAGGTTCGCTTAAGCAAAG TGCAGGTGGCGGCACCAAAAACAGGGATTGGTGGCCCAACATGCTCAACCTCGGCATCTT 40415 CCCGTCGAGGCGGCGGGAAACCAGGACTGGTGGCCCAACCGGCTCAATCTGAAGGTACT 10355 GCACCAAAACCCGGCCGTCGCTGACCCGATGGGTGCGGCGTTCGACTATGCCGCGGAGGT 210 TAAGAAGCTAGATCTGGCAGCGGTTAAAAAGGACCTGGCAGCGCTAATGACAGATTCACA 10295 CGCGACCATCGACGTTGACGCCTGACGGGGACATCGAGGAAGTGATGACCACCTCGCA 270 GGACTGGTGGCCAGCAGATTACGGTCATTATGGCCCCTTCTTTATACGCATGGCGTGGCA CAGCGCCGGCACCTACCGTATCGCTGATGGCCGTGGCGGTGGCTCCGGCTCACAGCG 0115 GTTCGCGCCCTTAACAGCTGGCCCGACAACGCCAGCTTGGACAAGGCGCGCCGGCTGCT TIGGCCCATCAAAAAAAAAAACGGTCGAAAAATCTCCTGGGCGGATCTAATGATACTCAC 10055 GTGGCCGGTCAAGAAGAAGTACGCCAAGAAGCTCTCATGGGCGGACCTGATTGTTTTCGC 510 AGGAAACGTAGCTCTGGAAACTATGGGCTTTAAAAACTTTTGGTTGCAGGTGGCAGAGC ACGCCAACATTCATCGCTATCGGACCCAAACGACCCGGGATTTTGACTATGCCGAAGAGTT Gaps Score 844.4; DB 24; Length 82993; Pred. No. 1.5e-252; 0; Mismatches 801; Indels 15; C Query Match 37.7%; Best Local Similarity 63.0%; Matches 1390; Conservative (

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2152629 CATTCGCGAGAGACTTTCGGCGCATGGCCCATGAACGACGCGCGCCTCATCGT 2152570
            The invention relates to evaluating strain variation within and between different populations of the tuberculosis becterial pathogen, whose proceed with the propertion of the tuberculosis or talated Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the first strain are positions in the consistence and the correspond to positions that differ in the nucleotide sequences of Mr. tuberculosis strains CDC 1531 (AA19963) and H3TRY (AA19963). The method is useful for evaluation strain variation of tuberculosis and has valuable application in the fields of the tuberculosis spendetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                         other;
                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from OSPYO ast segate. useboc gov/sequence.html?Docine62942881.
                                                                                                                                                                                                                                                                                                                                                                                                               2153346 TACAGAAACCACCAGCAGCGGCTAGCAACGGCTGTCCCGTCGTGGGTCATATGAAATA
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                                                                                                                                                                                                                                                                                                             Length 4403765;
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Pred. No. 1.6e-251;
0; Mismatches 801;
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63.0%;
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Matches 1390; Conservative
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                                             38804 GCCCTTCACCCCGGGCCGCACGGATGCGTCGCAGGAACAAACCGACGTGGAATCCTTTGC
                                                                                                                                                                            GTTTACAAATAAGCCGGGTCAGCTATCCAATGACTTCTTTGTAAACCTGCTAGACCTCAA
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          GCCTTTCAACCCGGGACGACGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTTCGA
                                                                                                                 38744 CGTGCTGGAGCCCAAGGCAGGTGGCTTCCGAAACTACCTCGGAAAGGGCAACCCGTTGCC
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                                                                                AGCACTAGAGCCAGCGGCTGACGGCTTTAGAAACTACATTAAACCGGAGCATAAAGTATC
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epidemiology; patient treatment; épidemic monitoring;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at directly from USPYO att sequence, html/Docid-6294328B1.
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     GGTGCTGGTAGGTGGCCTGCGCGGCTCCTCGGCGCAAACTACAGCGCTTACCGCTGGGCGT
                                                                                                GTTCACCGAGGCCTCCGAGTCACTGACCAACGACTTCTTCGTGAACCTGCTCGACATGGG
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                                                            GTTTACAAATAAGCCGGGTCAGCTATCCAATGACTTCTTTGTAAACCTGCTAGACCTCAA
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GGGTGGACACACCTTCGGAAAAACCCATGGTGCTGCCGATGCGGAGAAATATGTGGGCCG 869
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                                    AGAGCCTGCCGCGCAGGTATTGAAGAAATGAGCCTGGGGTGGAAAAACACCTACGGCAC
                                                                                                     1152512 GGAACCCGAGGCTGCTCGCTGGAGCAGATGGGCTTGGGCTGGAGAGAGCTCGTATGGCAC
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2155132 GAAATGGGACAACAGTTTCCTCGAGATCCTGTACGGCTACGAGTGGGAGCTGACGAAGAG 2155073 1290 1470 1767 1887 2067 1050 1170 1350 1410 2154715 1587 1947 1647 1707 1827 g 8 ö 유 ò g ò 원 ŏ ď à g ò g ö ď ò 셤 õ 셤 å 셤 ŏ a à g à g ð a δ 셤 ò g ò ð 2155430 2155370 2155847 2155787 2155727 2155667 2155607 CGAACCCGAGGCTGCTCCGCTGGAGCAGATGGGCTTGGGCTGGAAGAGCTCGTATGGCAC 2155193 2156086 TACAGAAACCACCACCGGAGCCGCTAGCAACGGCTGTCCCGTCGTGGGTCATGAAATA 2156027 2155967 2155907 TCAATGGAGCAATAACTTTTTGAAAACCTCTTTGGTTACGAGTGGGGAGCTTACCAAAAG 1049 ŝ 269 389 449 809 CATCTATGTAAACCCCGAAGGACCCAACGGCAAGCCAGACCCTATCGCTGCTGCGCGTGA 749 AGAGCCTGCCGCCGCAGGTATTGAAGAAATGAGCCTGGGGTGGAAAAACACCTACGGCAC 929 CGGACACGGTGCGGATACCATCACCAGTGGACTAGAAGGCGCCTGGACCAAGACCCCTAC 989 2155489 TGAGCGTTACAGCGGTAAGCGGGATCTGGAGAACCCGCTGGCCGCGGTGCAGATGGGGCT GATCTACGTGAACCGGGGGCCGAACGCCAACCGGACCCCATGGCCGCGGGGGGTCGA PACGTATAACACAAACACTGGCGGAAAATGCCCTTTTACCGGAGGTTCGCTTAAGCAAAG TGCAGGTGGCGCCCCAAAAACAGGGATTGGTGGCCCAACATGCTCAACCTCGGCATCTT ACGCCAACATTCATCGCTATCGGACCCAAACGACCCGGATTTTGACTATGCCGAAGAGTT TAAGAAGCTAGATCTGGCAGCGGTTAAAAAGGACCTGGCAGCGCTAATGACAGATTCACA CGCGACCATCGACGTTGACGCCCTGACGCGGGACATCGAGGAAGTGATGACCACCTCGCA GGACTGGTGGCCAGCAGATTACGGTCATTATGGCCCCTTCTTTATACGCATGGCGTGGCA CAGCGCCGGCACCTACCGTATCGGTGATGGCCGTGGTGGCGTGGCTCCGGCTCACAGCG TTGGCCCCATCAAAAAATACGGTCGAAAAATCTCCTGGGCGGATCTAATGATACTCAC 2155666 Greecegreaagaagracgecaagaagreecereareeecegaccrearge AGATGTATGGGAGCCTGAAGAAGATGTATACTGGGGAGCAGAAACCGAATGGCTGGGAGA 630 CAAGCGCTATGAAGGTGACCGAGAGCTCGAAAATCCCCTGGGAGCCGTACAAATGGGACT 750 TATTCGTGAGACTITTGGCCGAATGGCAATGAAGGAAGGAAGGAAGCGTGGCTCCTCATAGC GGGTGGACACACCTTCGGAAAAACCCATGGTGCTGCCGATGCGGAGAATATGTGTGGGCCG Gaps Length 4411529 G; 758379 T; 0 15; Score 844.4; DB 22; Length Pred. No. 1.6e-251; 0; Mismatches 801; Indels BP; 758565 A; 1449983 C; 1444602 Query Match 37.7%; Best Local Similarity 63.0%; Matches 1390; Conservative Sequence 4411529 210 570 066 90 150 270 330 2155786 390 810 2155309 870 2155252 930 2155192 ž 셤 à 쉽 셤 셤 용 à g ð 8 õ 셤 ð 요 ò g ð g ö 셤 õ 셤 ð g ŏ 윱 ð g ò à à ð

2154776 2154596 2154536 2154296 2154236 2154116 2154059 2154058 TGGCAAGGTGAAGTGGACCGGCAGCCGTGGACCTGGTCTTCGGGTCCAACTCGGAGTT 2153999 GGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCATCTATTAGAAA 1469 CTACCTGGGACCAGAAGTGCCTCAGGAAGACCTCATCTGGCAAGACCCTATACCAGATGT 1154655 TAGCGACAGGCGGCGCGCAAAGGTGGTGGCATCCGCCTGCAGCCAAAGTCGGGTG GGAGGTCAACGACCCCGACGGGGATCTGCCAATCGCACCCTGGAAGAGATCCA GCCTTTCAACCCGGGACGAGCGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTTCGA 2154355 CGTGCTGGAGCCCAAGGCAGATGGCTTCCGAAACTACCTCGGAAAGGCCAACCCGTTGCC 2154895 CGACGAGTTCGCCAAAGGCTACAAGCTGATCCACCGAGGACATGGGTCCCGTTGCGAG AGCACTAGAGCCAGCGGCTGACGGCTTTAGAAACTACATTAAACCGGAGCATAAAGTATC CGCTGAGGAAATGCTCGTAGACCGGGCGCAGCTTCTGTCGCTTTCGGCACCAGAAATGAC 2154295 GGCCGAGTACATGCTGCTCGACAAGGCGAACCTGCTTAGGCTCAGTGCCCCTGAGATGAC TGCTTTGGTAGGCGGTATGCGTGTACTGGGCACCAACTACGACGGTTCGCAGCATGGAGT GTTTACAAATAAGCCGGGTCAGCTATCCAATGACTTCTTTGTAAACCTGCTAGACCTCAAA 2154115 TATCACCTGGGAGCCCTCGCCAGCAGGATCACGGGACCTACCAGGGCAAGGATGGC---AG 1230 AGATGCTTTCGCGAAAGCATGGTACAAACTGACACACAGAGATATGGGACCAAAGGTGCG AAGCCATCCTCTTGTAGACGAAAACGATATTGAAGGCCTAAAAGCCAAAATCCTGGAATC CTCTGACAAGCGCGGCGGTGCCAACGGTGCACGTATACGACTGGCCCCACAAAAAGACTG 1530 GGAAGTAAACAACCCTCA---GCAACTTGCCAGGGTACTCAAAACACTAGAAGGTATCCA GGAGGACTTTAACCAGGCGCAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGATTGT GCTGGCCGGCTGTGCGGGTGTAGAAAAGCTGCAAAAGATGCTGGCCATGAGGTGCAGGT CACTAAATGGCGAGCCAGCGATGAATCAGACAAAGTTTTTGAAGGCAGAGACTTCAAAAC TGGCGAAGTAAAGTGGAGTGGCACCCGGGTAGACCTGATCTTCGGATCCAATTCCGAGCT CATGGACCCTGATTACGAAAAATTTCTCGACGGTACTATGAAAACCCTGATGAGTTTTGC **<b>TCCAGC**TGGAGCTTATCAGTGGAAACCAAAAGACGGTGCCGGGGCTGGCACCATACCGGA 1110 IGCACATGATCCCAGCAAGTCGCACGCTCCATTTATGCTCACTACGGACCTGGCGCTGCG

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                                                                                                                                                                                                                                                                           90 TGCAGGTGGCGGCACCAAAAACAGGGATTGGTGGCCCAACATGCTCAACCTCGGCATCTT
                                                                                                                                                                                                                                                                                                      273 CGCGACCATCGACGTTGACGCCCTGACGCGGGACATCGAGGAAGTGATGACCACCTCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 CGACCAGTGGGAGCC---CGATGAGGTTATTGGGGCCAAGGAAGCCACCTGGCTCGGCGA
Note: this sequence is not provided in the specification; it has been created by modifying the katg gene sequence given in Fig \gamma.
                                                                                                                                                                                                                                                                                                                                                                  150 ACCCCAACATTCATCGCTATCGGACCCAAACGACCCGGATTTTGACTATGCCGAAGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 TAAGAAGCTAGATCTGGCAGCGGTTAAAAAGGACCTGGCAGCGCTAATGACAGATTCACA
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                                                                                                                                                       15; Caps
                                                                                                           DB 20; Length 2331;
                                                                                                                                                    Indels
                                                              Sequence 2331 BP; 455 A; 735 C; 762 G; 379 T; 0 other
                                                                                                        Score 842.8; DB 20;
Pred. No. 5.8e-253;
0; Mismatches 802;
                                                                                                        Query Match
Best Local Similarity 63.0%;
Matches 1389; Conservative
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                                         2153998 GCGGGCGCTTGTCGAGGCTTATGGCGCCGATGACGCGCAGCCGAAGTTCGTGCAGGACTT 2153939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Invention realtes to a novel method of detecting Mycobacterium tuberculosis. The method comprises amplifying the BNA in the samples to generate a detectable amount of amplified DNA comprising a catalase to percoxide (tatG) DNA fragment with sequence of bases 944-1523 of the M. tuberculosis strain H378 WG katG gene sequence. The method optionally further comprises determining if the katG DNA fragment has a serie to threonine mutation in codon 315 (53157 method). Indicative of an isonicotinic acid hydraxide (IMN) reasistant W. tuberculosis strain. The especially human aputum, useful to diagnose tuberculosis. This disease is a major cause of human morbidity and mortality, and conclusive diagnosis and subsequent treatment depends on identification of the etologic agent W. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMB-resistant strains have emerged; the method allows such drug-resistant strains to be identified; the present sequence represents the M. tubercollosis kad gene variant.
              2127 AAGAGCCCTCGCAGAAGTGTACGGCTGTGCAGATTCTGAAGAAAAGTTTGTTAAAGATTT
                                                                                                                            Catalase-peroxide; katG; mutation; isonicotinic acid hydrazide;
                                                                                                     2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of Mycobacterium tuberculosis - by amplifying kato
and detecting specific fragment, and optionally identifying
narr-resistant strains by detecting specific mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product = "catalase peroxide variant"
/note = "the start codon is not indicated"
                                                                                                  2187 TGTGAAGGCCTGGGCCAAAGTAATGGACCTGGACCGGTTTGATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compared to
                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis catalase peroxide (katG) gene variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; detection; variant; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G to C variation as wild-type katG gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                    AAX00818 standard; DNA; 2331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                    29-MAR-1999 (first entry)
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/note- '
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P-PSDB; AAW95399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INH; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variation
                                                                                                                                                                                                                                                                                          AAX00818;
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90 TGCAGGTGGCGCACCAAAAACAGGGATTGGTGGCCCAACATGCTCAACCTCGGCATCTT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This partial DNA sequence encodes the katG gene of Mycobacterium tuberculosis strain #737W within is used in a novel method to rapidly defaulty strains of M. tuberculosis Which are resistent to isoniazid (INM, isonicotinic acid Mydraxide). The method involves the use of restriction fragment length polymorphism (RTEP) analysis to determine if a Ncil-Mspi restriction site is absent in the DNA of the strain at the coden corresponding to codon 450 fg M. tuberculosis katG gene consensus sequence (see ANWI343). The absence of the site indicates an engagement of the strain at the coden while the second set of a M. tuberculosis katG gene an engagement of the strain at the coden while the second second
         30 IACGTATAACACAAAACACTGGCGGAAAATGCCCTTTTACCGGAGGTTCGCTTAAGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 TACAGAAACCACCACCGGAGCCGCTAGCAACGGCTGTCCCGTCGTGGGTCATATGAAATA
                                                                     2127 AAGAGCCCTCGCAGAAGTGTACGGCTGTGCAGATTCTGAAGAAAAGTTTGTTAAAGATTT
                                                                                                   GCGGGGCCTTCTCGAGGTCTATGGCGCCCATGACGCGCAGACTTCGTGCAGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determination of isoniazid sensitivity of Mycobacterium tuberculosis strains - by restriction length polymorphism analysis of katG gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19; Length 2235;
                                                                                                                                                                                 2187 TGTGAAGGCCTGGGCCAAAGTAATGGACCTGGACCGGTTTGATCTG 2232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculosis; katG gene; isoniazid resistance; isonicotinic acid hydrazide; ss.
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Pred. No. 1e-249;
0; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis partial katG gene
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85..2235
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Best Local Similarity 63.0%;
Matches 1389; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This partial DNA sequence encodes the ARIC gene from a variant strain of Mycobercarium tuberculosis H37Rv which is used in a novel method to rapidly identify strains of M. tuberculosis which are resistant to rapidly identify strains of M. tuberculosis which are resistant to rapidly identify strains of Form as isonicaterine dead hydrazide). The method involves the use of restriction fragment length polymorphism (RPLP) analysis to determine if a wolf-shelp respirator is strain at the codom corresponding to codom 45 of a M. tuberculosis katch gene consensus sequence (see AAV31343). The absence if he site indicates an IMM-resistant strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of isoniazid sensitivity of Mycobacterium tuberculosis strains - by restriction length polymorphism analysis of katG gene
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                                                                                                                Mycobacterium tuberculosis strain H37Rv variant partial katG gene
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0; Mismatches 842;
                                                                                                                                                    Tuberculosis; katG gene; isoniazid resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The katc gene of Mycobacterium tuberculosis was isolated on a KpnI fragment by shought cloning, the sequence conclains one open reading frame with high coding probability; a 73 mains acid protein last encoded by the CoRP having predicted mol.w. 180032. This protein conforms to the structure of known betterial cetalase-peroxidases which consist of two modinas (possibly the result of a diplication event), books showing homology to the yeast enzyme, fused to a unique the kniff agene on result in loss of IMHI-susceptibility, i.e. the formation of all presides, when the formation of a formation of modified to the formation of a formation of milbour esistent Mycobacterial strains
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isoniazid, rifampicin or streptomycin resistance in tuberculosis
by detecting mutation in katć, rpoB or rpsi genes
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  Location/Qualifiers
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Matches 1335; Conservative
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1408 TCGGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCATCTATTAGA 1467
                                                                  1468 AACTCTGACAAGCGCGGCGGTGCCAACGGTGCACGTATACGACTGGCCCCACAAAAAGAC 1527
                                                                                                                                                                                                                                    1576 GAGTCATTCA-----CTCGGCGGGGAACATCAAAGTGTCCTTCGCCGACCTCGTGTG 1629
                                                                                                                                                                                                                                                                     1648 CTGGCCGCCTGTGCGGGTGTAGAAAAGCTGCAAAAGATGCTGGCCATGAGGTGCAGGTG 1707
                                                                                                                                                                                                                                                                                        CCTTTCAACCCGGGACGAGCGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTTCGAA 1767
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                                                                                    1528 TGGGAAGTAAACAACCTCAGCAACTTGCCAGGGTACTCAAAACACTAGAAGGTATCCAG
                                                                                                                                                                     1516 TGGGAGGTCAACGACCCCGACGGATCTGCGCAAGGTCATTCGCACCCTGAAGAGATCCAG
                                                                                                                                                                                                   GAGGACTTTAACCAGGCGCAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGATTGTG
                                                                                                                                                                                                                                                                                                                                                                                                         1768 GCACTAGAGCCAGCGGCTGACGGCTTTAGAAACTACATTAAACCGGAGCATAAAGTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                             750 GTGCTGGAGCCCAAGGCAGATGGCTTCCGAAACTACCTCGGAAAGGGCAACCGTTGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1396 TCGGGATTGACTGTCTCACAGCTAGTTTCGACCGCATGGGCGGCGGCGCGTCGTTCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis (strain H37Rv).
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  2422 GTGGCCGGTCAAGAAGAAGTACGGCAAGAAGCTCTCATGGGCGGACCTGATTGTTTTCGC 2481
                                                                                                                                         2542 CGACCAGTGGGAGACC----GATGAGGTCTATTGGGGCAAGGAAGCCACCTGGCTCGGC 2596
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                                    510 AGGAAAC -- GTAGCTCTGGAAACTATGGGCTTTAAAACTTTTGGTTTTGCAGGTGGCAGA 567
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                                                      568 GCAGATGTATGGGAGCCTGAAGAAGATGTATACTGGGGAGCAGAAACCGAATGGCTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCACCAAAACCCGGCCGTCGTGACCCGATGGTGCGGCGTTCGACTATGCCGCGGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding catalase-peroxidase HPI - useful for rapid identification of isoniazid resistant Mycobacterium tuberculosis
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Pred. No. 7.9e-215;
0; Mismatches 842;
/*tag= a
/gene= "katG"
/product= "catalase-peroxidase"
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92US-0875940.
92US-0929206.
93US-0029655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 CATCGCTATCGGACCCAAACGACCCGGATTTTGACTATGCCGAAGAGTTTAAGAAGCTAG
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                                                                                                                                                                                  Sequence may be used to construct plasmid pobl0 used to transform E.coll UM28. The transformed expression system may be used to produce heat resistant peroxidase in large quantities.
                                                                                                                                                                                                                                                                                         Score 721.6; DB 11; Length 2195;
Pred. No. 5.7e-215;
0; Mismatches 754; Indels 42;
                                                                     DNA contg. genetic information of heat resistant peroxidase prepd. by culturing transformant and collecting heat resistant
                                                                                                                                                                                                                                                          Sequence 2196 BP; 576 A; 564 C; 633 G; 423 T; 0 other
                                                                                                                                              Disclosure; Fig 2; 8pp; Japanese.
                                                                                                                                                                                                                                                                                               32.2%;
                                                                                                                                                                                                                                                                                                              Best Local Similarity 62.7
Matches 1336; Conservative
            WPI; 1990-372008/50.
                                 P-PSDB; AAR08205
                                                                                             prepd. by peroxidase
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                                                                                                                                                                                                                                                                                                           GCTGAGGAAATGCTCGTAGACCGGGCGCACCTTCTGTCGCTTTCGGCACCAGAAATGACT 1887
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            GAGGACTTTAACCAGGCGCAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGATTGTG
                                                                                                                                                                                                                                                          TITACAAATAAGCCGGGTCAGCTATCCAATGACTTCTTTGTAAACCTGCTAGACCTCAAC
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| CTGCTGGGGGACAAGGTACTCGACGTTCAATCTG 2232
| CTGCTGGGGGAAAGGTGAACTCGAACAGTTCAACTG 4180
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/*tag= a
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1898 TCGGGGTGCTGACCAACGACTTCTTTGTCAACTTGTTGGATATGAACTATGAATGGGTGC 1957
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                                                                                                                                                       2012 GGACGGCGCGGGGGGGATCTCATTTTCGGATTTTACGCCCAAGACGACAACAAGAAG
                                                                                                                                                                                                                                            CCAGCGATGAATCAGACAAAGTTTTTGAAGGCAGAGACTTCAAAACTGGCGAAGTAAAGT
                                                                                                                               GGAGTGGCACCCGGGTAGACCTGATCTTCGGATCCAATTCCGAGCTAAGAGCCCTCGCAG
                                                                                                                                                                                                                       AAGTGTACGGCTGTGCAGATTCTGAAGAAAGTTTGTTAAAGATTTTGTGAAGGCCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcaligenes (Deleya) aquamarinus catalase-64CA2 gene
                                                                                                                                                                                                                                                                                                            2201 CCAAAGTAATGGACCTGGACCGGTTTGATCTG 2232
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CCCGGGCATGGTTCAAGCTTACCCATAGGGATATGGGACGAAAACGAGATATCTCGGCC
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                                                                                                          905 GCGATACGATCACAAGCGGCATTGAAGGCGCTTGGACGCCGACGCCAACCCAGTGGGATA
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Best Loc Matches	Similarity 59.5%, pred. No. 1.8e-199; 7; Conservative 0; Mismatches 808; Indels 60; Gaps	qa XX	1167 GGTTGACGCCAGCGACCCCTCTAT
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	159 TICATOGCHAUCGGACCCAAACGACCGGATTTGACHAGGCGAAGAGTTAAGAGCT 218 210 AGATGCCAAAATCAGACCGATGATCGATGATTCAATAACAGAAGAAGAACAAGAACAAGAACAAACA	A G	1224 GITTGCAGATGCTTTCCCGAAAGC 
o,	AGATCTGGCAGCGGTTAAAAGGACTGGCAGCGCTAATGACAGATTCACAGGACTGGTG	දුරු පු	1284 GGTGCGCTACCTGGGACCAGAAGT
a k	270 CGATTTCGACGCGCTGAAGAAAGATGTCCACGCGTTGATGACGACGATAGCCAAGAGTGGTG 329 279 GCCAGCAGAATAAGGGTCATTATGGCCCCTTCTTTATACGCATGGCGTGGCACAGGCGCGG 338	ō	1344 AGATGTAAGCCATCCTCTTGTAGA
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op.	Caagaagaagtacggcaacaaaatcagctgggcagacctgatgattctggctgg	ογ	1584 CCAGGAGGACTTTAACCAGGCGCA
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:	GGAGCCTGAAGAAGATGTATACTGGGGAGCCAGAACCGAATGGCTGGAGACAA	, y 8	1644 TGTGCTGGCCGGCTGTGCGGTGT 
	GGAACCCGAAAAAGATATCTACTGGGGTGACGAAAAAGAGTGGCTGGC	λō	1704 GGTGCCTTTCAACCCGGGACGAGC
è a	633 GCGTPACGACGTCACCGACGCTCCANANTCCCTGGGACCCGTACAAT 683 	ପ୍ର	
ō	GGGACTCATCTATGTAAACCCCGAAGGACCCAAGCCAAG	ζo	1764 CGAAGCACTAGAGCCAGCGGCTGA
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oy qa	744 GCGTGATATTCCTGAGACTTTTGGCCGAATGGCAATGAATG	<b>3</b> €	1824 AICCGCIGAGGAAIGCICGIAGA 1851 GAAGCCGGAAGAGAIGCICGIGGA
	804 CATAGOGGGTGGACACACATCGGAAAAACCCATGGTGGCGATGGGGAAAATATGT 863	šo t	1884 GACTGCTTTGGTAGGCGGTATGCG
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ko d	864 GGGCCAGAGCCTGCCGCCGCAGGTATTGAAGAATGAGCCTGGGGTGGAAAAACCTA 923	3 B	1971 CGTATTCACCGATTGTGAAGGCCA
9 8	947 AUCUCUTARUCURANGUCTUTGANGTTRAAAACURGGGCTTAGGTTGGGGGCAACCCCAA 986 994 AGGGAACAGAAAGGTGGGGATAAAAAAAAAAAAAAAAAA	δŏ	2004 CAACACTAAATGGCGAGCCAGCGA
. 4	CATGCAGGGAAGGCAAGCCCGTGACCTCGGGTATCGAAGGTGCTTGGACCACCAA	qq	2031 GGGGAACAGCTGGAAGCC
٥y	984 CCCTACTCAATGGAGCAATAACTTTTTGAAAACCTCTTTGGTTACGAGTGGGAGCTTAC 1043	à f	2064 AACTGGGGAAGTAAAGTGGAGTGG 
D <b>b</b> 1	TACAAT	3 8	2124 GCTAAGAGCCCTCGCAGAAGTGTA
	1004   CAAAAGTCCAGCTGGAGCTTATCAGTGGAAACCAAAGAGGCGGGCG	a d	2145 ACTGCGCTCTTACGCAGAAGTGTA
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1643 ACCGGGCGCACCTTCTGTCGCTTTCGGCACCAGAAAT 1883 1463 GTGCCAACGTGCACGTATACGACTGGCCCCACAAA 1523 1574 1616 TCTCTGCCGACACCGGCGCTAGCATCGCGGACGTGAT 1670 1703 CCTCGCGGGTGGATCTGGTATTTGGTTCCAACTCGCT 2144 CATGGTACAAACTGACACACAGAGATATGGGACCAAA 1283 1406 ACGAAAACGATATTGAAGGCCTAAAAGCCAAAATCCT 1403 AGCAACTIGCCAGGGTACTCAAAACACTAGAAGGTAT 1583 CGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTT 1763 ACGCCTTTAGAAACTACATTAAACCGGAGCATAAAGT 1823 TICGCCACAACCCGAICAIGACCGAIGCGGAIAIGGC 1226 TGCCTCAGGAAGACCTCATCTGGCAAGACCCTATACC TGCCGGCAGAAGACCTGATTTGGCAAGACCCGATTCC GCGATGCGACCGCGAGATGACCGACGCAGACTCCTT AGCTATCCAATGACTTCTTGTAAACCTGCTAGACCT ATGAATCAGACAAAGTTTTTGAAGGCAGAGACTTCAA CGGTAGGTAGCAACGCCTACGAAATCCGCGAAA GCACCCGGGTAGACCTGATCTTCGGATCCAATTCCGA ACCCCTGTGCAGATTCTGAAGAAAAGTTTGTTAAAGA AAAAAATTTCTCGACGGTACTATGAAAACCCTGATGA ACCTGGTAAGCACGCCATGGGCTTCTGCATCTACTTT AGCGCCTGGCGAAAGTGCT------AATCAGATAACAAAGCAGTATCGTTGGCCGACCTGAT TAGAAAAAGCTGCAAAAGATGCTGGCCATGAGGTGCA 2205 CTTCGTCGCCGCCTGGACCAAAGTGATGAACGCCGACCGTTTCGA 2249 TAATGGACCTGGACCGGTTTGA 2228

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to the DNA and protein sequences of a novel to the inveal control and actalase polypetide. The protein of the invention or its homologue is useful for catalysing the breakdown of hydrogen perceited. The protein sequence of the invention is useful for modifying amail molecule. The protein of the invention is amail molecule. The protein of the invention is also useful for catalysing biochemical reactions, for hydrolysing also useful for catalysing biochemical reactions, for hydrolysing specifically to the protein. The nucleat act of sequences of the nucleat ample, such as a soil sample, contains an organism having the nucleat act of such as a soil sample, contains an organism having the nucleat act of solating related nucleic acids. An antibody that binds the cellulase protein of the invention is useful in immunoffinity the culturase protein of the protein of the invention is useful in immunoffinity in the independence to isolate or purity the protein or for detection of protein of invention is beet table, is heat resistant, and is able to the invention and regain activity after exposure to temperatures of from about 60 to 105 degress in his present sequence encoding the hardlegment assumes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified catalase polypoptide useful for catalyzing the breakdown of hydrogen peroxide, for modifying small molecules, and for generating antibodies which bind to the polypeptide.
                                                                                                                         Gene; ss; marine bacteria; catalase; hydrogen peroxide; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2262 BP; 553 A; 612 C; 663 G; 434 T; 0 other;
                                                                                                 DNA encoding Alcaligenes catalase protein 64CA2
                                                                                                                                                                                                             /*tag= a
/product= "Catalase protein"
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                                                                                                                                                                                 Location/Qualifiers
           ABS53944 standard; DNA; 2262 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 5; 44pp; English.
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97US-0951844.
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                                                                                                                                                                                                                                                                                                                                             390 CACCTACCGTATTGCTGATGCCGTGGGGGGGGGGGGTGTACCGGAAGCCACGCTTTGCAC
                                                                                                                                                                                          270 CGATTTCGACGCGCTGAAAAAAATGTCCACGGTTGATGACGATAGCCAAAGAGTGGTG
                                                                                                                                                                                                                                                               570 GGCTTATGAGTCCATGGCTTACTGCTTACGGCTTCTTTCGGCCGCGTCGATATTG
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                                    150 CGGTACTTCCAACAAAGATTGGTGGCCGGAAGGGTTGAACCTGGATATTTTGCATCAGCA
                                                                           159 ITCAICGCIAICGGACCCAAACGACCCGGATTITGACTAIGCCGAAGAGTTIAAGAAGCI
                                                                                                                                                           219 AGATCTGGCAGCGGTTAAAAAGGACCTGGCAGCGCTAATGACAGATTCACAGGACTGGTG
                                                                                                                                                                                                                                         279 GCCAGCAGATTACGGTCATTATGGCCCCTTCTTTATACGCATGGCGTGGCACAGCGCCGG
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                                                                                                                  210 AGATCGCAAATCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCT
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Query Match 30.0%; Best Local Similarity 59.5%; Matches 1277; Conservative

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2205 TTTTGTGAAGGCCTGGCCAAGTAATGGACCAGGACGTTTGA 2249
2205 CTTCGTCGCCGCCTGGACCAAAGTGAAGAAGACAAGAACGACGACGATTCGA 2249
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APPLICANT: Robertson, Dan E. APPLICANT: Subertson, Dan E. APPLICANT: Sangal, Indicalit APPLICANT: Sangal, Indicalit South Structure of Inventors Carladass Number of Scourscendences: 8 CORRESPONDENCE ADDRESS: 8 ANCHARGSON
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FILMS DATE: 03-011-1996
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Live 0; Mismatches
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REFERENCE/DOCKET WINNER: 09015/002001
FELECOMMUTCATION INFORMATION:
FELEPHONE: 619/678-5070
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08674887A Patent No. 5939300
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ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
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Matches 2238; Conservative
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STRANDEDNESS: double
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MEDIUM TYPE: Diskette
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sequence 7, App. 11
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Sequence 7, Appli
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                                                                                                                                                                               October 8, 2003, 07:56:28 ; Search time 126.323 Seconds (without alignments) (without alignments) (% 189.780 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-757-653-147
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Oy 2221 CGGTTGATCTCAAATAA 2238  Db 2221 CGGTTGATCTCAAATAA 2238	čo da	301 GGCCCTTCTTATAGCATGGCTGGAAAGGCGCGCACTGCTGTATGGTTGGC 360 301 GGCCCTTTTTATAGCATGGCTGGAAAGGCGGGCCTACCTTACGTTATAGGTGGAAGGAA
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; Sequence 7, Application US/08951844 ; Patent No. 6074860 ; GENERAL INFORMATION:	ob i	421 GCCANTCHGARDAGCACGCTTGCTTGTGCCCATCAAAAAAAAAAAAA 480
; APPLICANT: Kobertson et al. ; TITLE OF INVENTION: Catalases ; NUMBER OF SEQUENCES: 8	e k	
CORRESPONDENCE ADDRESS: ADDRESSES: CARELA, BYRNE, BAIN, GILFILLAN,	qa	481 ATCTCCTGGGCGGATCTAATGATACTCACGGAAACGTAGCTCTGGAACTATGGGCTTT 540
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COUNTRY: C ZIP: 07068 COMPUTER REAL MEDIUM TYPE	6 da	601 regerracheanacchartectregergachachactrachachachachachachachachachachachachacha
COMPUTER: IBM PS/2 OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA:	. yo	661 ANTOCCCEGEGRACOGERCANATOGGRACICATCINTGTAACCCCGAAGGGCCCAAGGGC 720 [61] ANTOCCCCGAAGGGGGTACAATGGGACTCATCTATCTAAACCCCCAAGGACCCAAGGGC 720
	Qy	721 AAGCGAGACCCAATGGCTGCTGCGGGTGATATTGGTGAGACTTTTGGCCGAATGGCAATG 780
•	do da	781 ANTGACGAAGAAACOCTGCTCATAGCGGGTGGACACACCTTCGGAAAAACCCATGGT 840 181 ANTGACGAAAACCGTGCTCTCAAAGCGGTGGAACACCTTCGGAAAACCATGGT 840
RECISTRATION NUMBER: 28,019 REFERENCE/DOCKET NUMBER: 331400-55 TELECOMMULI TEDERATION: TELECOME. 201-994-1700	QY	841 GCTGCCGATGCGGAGAAATATGTGGCCCGAGAGCCTGCCGCCGCAGGTATTGAAGAAATG 900
INFO	ος	901 AGCCYGGGGTGGAAAAGACCTACGGCACCGGACACGGTGGGGATACATCACGGTGGA 960 
; TYPE: NUCLEIC ACID ; STRANDENESS: SINGLE ; TOPOLOGY: LINEAR ; MOLECULE TYPE: DNA	λΌ qα	961 CTAGAAGGCGCCTGGACCAAGACCCTACTCAATGGAGTATAACTTTTTTGAAAACCTC 1020 
100.0%; Score 2238; DB 3; Length 2238; 100.0%; Pred. No. 0;	oy da	1021 TTTGGTTACGAGTGGGAGCTTACCAAAAGTCCAGCTGGAGCTTATCAGTGGAAACCAAAA 1080 
Matches 2238	oy Db	1081 GACGGTGCCGGGGCTGCCACCATACCGGATGCACATGATCCCAGCAAGTCGCACGCTCCA 1140 
1 ATGGAAATCACAGACTTCAGAATCACATAGACAAAAAACAGAAAAACAGAAAAAAAA	QV QV	1141 TTTATGCCTACTACGCGCCTGCCTCCCACCCCTGCTACAAAAATTCTCGA 1200 1141 TTTATGCCCTACGCACCTGGCGCTGCGCATGGACCCTGATTACGAAAAATTCTCGA 1200
61 CCFFTPACCGAGGFTCCCFTAAGCAAAGTCAAGTGCGGCACACAAAAAAGGGTTCG 121 TGGCCCCAAAAGTGCTCACCCGGGAGTTCACCCCAAATTCATCCGCAAACTTCATCCCAAACTTCATCCCAAACTTCAACCAAACTAATTCAAACAAACAAAACAAAACAAAAAA	& a	1201 CGGTACTATGAAAACCTGATGAGTTTGCAGATCTTGCCGAAAGCAAGGATGGTAAACTG 1260 1201 CGGTACTATGAAAACCTGATGAGTTTGCAGATGCTTTGCGGAAAGCAGGGTAAACTG 1260
121 TGGCCCAACATGGTCAACCTGGCATGCTTAGGCAACATGTCATGGTTATGGGCTATGAACTTAACAGGTTAAGGAGGCAACATAACAGGCAACATTAAGATGAACAGATGGCAAGGGGGGGG	₹ 60 m	1261 ACKACAGAGAGATATGGGACCAAAGGTGCGCTACCTGGGACCAGAAGTGCCTAGAAGAACAC 1320 1261 ACACAGAGATATGGGACCAAAGGTGCGCTACCTGGGACCAGAAGTGCCTCAGGAAGAC 1320
	o <sub>y</sub>	1321 CTCATCTGGCAGACGCCTATACCAGATGTAAGCATCCTCTTGTAGAGGAAACGATATT 1380

1te 1400

11on 2.0

	MEDIUM TYPE: Diskette COMPUTRE: THE COMPATIDE COMPUTRE: TRANCOMPATIDE SOFWHARE: RealESD for Mindows Version SOFWHARE: RealESD for Mindows Version FILLING DATE: FILLING DATE: RECOMPATICATION NUMBER: US/09/412,347 FILLING DATE: APPLICATION NUMBER: OS/09/412,347 APPLICATION NUMBER: OS/09/412,347 APPLICATION NUMBER: OS/09/412,347	FILING ANTE: NOTE NOTE NOTE NOTE NOTE NOTE NOTE NOTE	JENUTH: 2336 Dase pairs TYPE: noticied eaid STRANDENESS: double STRANDENESS: double STRANDENESS: DAN HOLECULE TYPE: COAID NAME/KET: COAID Sequence UCATION: 12235	Ouery Match 100.0%; Score 2238; Best Local Similarity 100.0%; Pred. No. 0; Matches 2238; Conservative 0; Mismatches Qy 1 ATGGARANTCACAACACTCAGGATCTTCTACGT	09 61 CCTTTACCGGAGGTTCGCTTAAGCAAAGTGCAGG Db 61 CCTTTTACCGGAGGTTCGCTTAAGCAAAGTGCAGG Q9 121 TGGCCCAACATGCTCAACCTCGGCATCTTACGCC Db 121 TGGCCAACATGCTCAACCTCGGCATCTTACGCC Db 121 TGGCCAACATGCTCAACCTCGGCATCTTACGCC	0   181 GACCGGGATFTFGACTATGCCGAAGAGTTAAGAA   181   11   11   11   11   11   11	0y 301 09CCCCTTCTTATACCCATGGCGTGCGAAGGCGTGCGAAGGCGC  Db 301 GGCCCTTTATACCCATGGCGTGCCAAGGCGC  Oy 361 CGTGGTGGCGTGGCTTCAAAGGCTTCAAAGGTTGCGTTGCGTTGCGTTGGCGTTGGCGTTGGCTTGGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGGTTGGGTTGGGTTGGTTGGTTGGGTTGG
DECATCTGGGAAGACCTATACCAGATGTAAGCCATCCTCTTGTAGACGAAACGATATT 1380			1,41 1801 1801 1861		2041 2041 . 2101 . 2101		REGULT 3  10-9412-347-7  10-9412-347

ö AAGAAGCTAGATCTGGCAGCGGTTAAAAAG 240 AGCGCCGGCACCTACCGTATCGGTGATGGC 360 Gaps ö DB 4; Length 2238; 0; Indels 138; DI 0, 0; ches oy oy g

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750 TATTCGTGAGACTTTTGGCCGGAATGGCAATGAATGACGAAGAAGCGTGGCTCTCATAGC 809
                                                                                                                    990 TCAATGGAGGAATAACTTTTTGAAAACCTCTTTGGTTAGGAGTGGGAGCTTACCAAAAG 1049
                                                                                                                                                                                                                                                                                                                   1047 CAANTGGGACAACAGTTCCTCGAGATCCTGTACGGTACCGTGCGAGCTGACAACAGAAAA 1106
                                                                                                                                                                                                                                                                                                                                                                                1107 CCTGCTGCGGCTTGGCAATACACGCCCAAGGACGGGCGCGGTGCGGGGACACATCCCGGA 1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1144 ATACCTTGGGCCGCTGGTCCCCAAACAACACCTGCTGCTGCGAACCAGCTCCCTGCGGATCGGATCGGTCCCTGCGGT 1403
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                                                        GGGTGGACACACCTTCGGAAAAACCCATGGTGCTGCCGATGCGGAAAAAATATGTGGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2331;
                                                                                                                                                                                                                                                                                                                                                   Score 844.4; DB 1; Length
Pred. No. 5.4e-251;
0; Mismatches 801; Indels
                                                                                         150.141051
CLASSIFICATION. 435
ATTORNEY/AGENT INFORMATION:
NAME: WOOSSIGE, WARTEN D.
NAME: WOOSSIGE, WARTEN D.
NAME: WOOSSIGE, WARTEN D.
NEGIZERATION WINDER: 130,440
TREPERNOK-COCKET WINDER: 150,140
TREPERNOK 1612-399-391
INFORMATION POR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 base parts
TYPE: nicited cafe as STRANDERISTICS:
TYPE: nicited cafe as STRANDERISTICS
TOPPOLYCENERS
T
                                                                                                                                                                                                                                                                                                                                          Query Match 37.7%;
Best Local Similarity 63.0%;
Matches 1390; Conservative (
                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 70..2289
US-08-418-782-20
                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
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                                                           15;
                       2331;
                       Length
                                                             Indels
                                                           0; Mismatches 801;
                       Score 844.4; DB 2;
Pred. No. 5.4e-251;
                       37.78;
                    Query Match
Best Local Similarity 63.09
Matches 1390; Conservative
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GITTACAAATAAGCCGGGTCAGCTATCCAATGACTTCTTTGTAAACCTGCTAGACCTCAA 2006
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                                                                                                                                                                  2004 GITCACCGAGGCCTCCGAGTCACTGACCAACGACTTCTTCGTGAACCTGCTCGACATGGG
                                                                                                                                                                                                                                                                                                   TGCTTTGGTAGGCGGTATGCGTGTACTGGGCACCAACTACGACGGTTCGCAGCATGGAGT
                                                                             2007 CACTAAATGGCGAGCCAGCGATGAATCAGACAAAGTTTTTGAAGGCAGAGACTTCAAAAC
                                                                                                                                                                                                                                                                              TGGCGAAGTAAAGTGGAGTGGCACCCGGGTAGACCTGATCTTCGGATCCAATTCCGAGCT
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APPLICANT: Aline Bruce C.
APPLICANT: Aline Bruce C.
TITLE OF INVENTION: Detection of Isoniazid Resistant Strains
TITLE OF INVENTION: of M. Tuberculosis
NUMBER OF SEQUENCES: 22
NUMBEROUNDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2187 TGTGAAGGCCTGGGCCAAAGTAATGGACCTGGACCGGTTTGATCTG 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUDRESSEE: Wueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 5922375th Fourth Street, Ste. 203
CITY: Mineapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Flooppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin TR-PELICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230.00010130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/852,219
FILING DATE: 07-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08852219 Patent No. 5922575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Sandberg, Victoria A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEPAK: 612-305-1228
INFORMATION FOR SEC ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2331 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: 70...
US-08-852-219-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55401
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US-08-852-219-20
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                                                                                                                              1947
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Db 2181 GCGGGCGTTPTCGGGGGCCGATGACGCGCGCGCGCGCGAAGTTCGTGCAGGACTT 2240  Qy 2187 TGTGGGCCCAAAGATAATGACCTGGACGCTTTGAACTT 2232  Db 2241 CGTCGCTGGCCTAGGACTATAAACTGACGAGTTCGACGT  Db 2241 CGTCGCTGCGCTGGGACAAGGTGATGAACGTGCAGGTTCGACGTG 2286	RESULT 6 19-09-103-19-40A-2/C 19-09-103-19-40A-2/C 19-09-103-19-103-10-40A-2/C 19-09-103-10-40A-2/C 19-09-103-10-40A-2/C 19-09-103-10-40-40-40-40-40-40-40-40-40-40-40-40-40	in order invocation: The bases at various positions throughout the sequence in	2153226 GAGCAAAACCGGGCGTACGAACGACCGAAACCCGGAAGATTTACAACCCGAAGATT 209     2153226 GAGCAAAACCGGGCGTCGACCCGATGGGTGCGGCGTTCGACTATGCCGAAGATT 215167     210 TAAGAAGCTGGCTGACCGTTACAGGGCGTGGCGCGTTAGACGCGGAAGTTTACA 269     210 TAAGAAGCTGGCTGGTGACGGTTAAAAAGGACCTGCACTAATGCCGCGAATTACAC 269     210 TAAGAAGCTGGCTGGCTGACGGTTAAAAACGACGCGCGCTGAATCACGCGCTGAATTACACGAAGAACTTATACCGCAATCACGACGTGAAAATCACGACGAAACTACGAAAATCACGAACGA
1050 TCCACCTGAACTTATCAGTGCAAACCAAAAGCGGTGCCGGGGCTGGCACCATACCGGA   1109	1170 CARGAGACCTGANAMATTCTCGACGGTACTARGAMACCCTGATGAGTTGC 1229 1124 GGTGGATCCCTGATAACGAAAAATTCTCACGGTGCTGCTGAAACCCTGATGAGTTTGC 1229 1124 GGTGGATCCGATACGGTCAAACGTGCTGCACACGGTGAAATTGC 1233 1230 AGATCCTTCGCCAAACGGTCAAACGTGCACACACGAAATTGGCCAAATTGGC 1283 1290 AGACGTTCGCCAAAGGCTGAAACGTGAATCACCGAAATTGGTCCCAAGGAATTGGTCCCAAGGAATTGGTCAAGGTTCCAAGGTTCAAGGTTCAAGGAATTGGTCAAGGTTCCAAGGTTCAAGGTTCACCAAGAGTCCTCAAGAATGGTCAAGGTTCAAGGAATTGGTCAAGGTTCCAAGGTTCAAGGTTCACCAAGATCCACGAATCCACGAATTGGTCAAGGTTCAAGGTTCAAGAAAACGAAAAATTGAAGGCCAAAAAGGTTAAGAATTGAAGGCAAAAAAAA	1530 GGAAGTAAACAAGCCTCAGCAACTTGCCAGGGTACTCAAAACCTAGAAGGTATCCA 1586	1767   ACACTAGAGCAGGCGTGAGGCTTTAGAAACTACATTAAACCGGAGCATAAGTATC 1926

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Db 2154955 GGTGGATCCGATCTATG	ò	Db 215		47   LD Z154835 ATACCTTGGGCCGCTGG	OY 1350 AAGCGATCCTCTTGTAG	δō	Db 215	Oy 1470 CTCT	Db 2154655 TAGCGACAAGCGCGGCG	OY 1530 GGAAGTAAACA	Db 2154595 GGAGGTCAACGACCCG				Db 2154475 GCTCGGTGCCTGTGCCG	Qy 1707 GCCTTTCAACCGGGGAC	3	OY 1767 AGCACTAGAGCCAGGGG   1	OY 1827 CGCTGAGGAAATGCTCGT	Db 2154295 GGCCGAGTACATGCTGCT	QY 1887 TGCTTTGGTAGGCGGTAT	Db 2154235 GGTGCTGGTAGGTGGCCT	Qy 1947 GTTTACAAATAAGCCGGG	Db 2154175 dricaccaagccrccaa	OY 2007 CACTAAATGGCGAGCCAG	Db 2154115 TATCACCTGGGAGCCTC	Qy 2067 IGGCGAAGTAAAGTGGAG	DD 2154058 TGGCAAGGTGAAGTGGAC	Qy 2127 AAGAGCCCTCGCAGAAGT	Db 2153998 GCGGCGCTTGTCGAGGT	Qy 2187 TGTGAAGGCTGGGCCAA	Db 2153938 CTCGCTGCGACAAK	RESULT 8 US-08-418-782-1
2156026 CCCCTCGAGGCGGCGGAAACCAGGACTGTGGCCCAACCGGTCGAACTTGAAGTTATTTGAAGTTATTTTAAACTTAAACTTAAACTAAACTAAACTAAACTAAAACTAAAACTAAAAAA		2155966 GCACCAAAACCCGGCCGTCGCTGACCCGATGGGTGCGGCGTTCGACTATGCCGCGGAGGT 2155907	210 TANGANGCTAGATCTGGCAGGOGTTAAAAAGGACCTGGCAGCGCTAATGACAGATTCACA 269	90800	270 GGACTGGTGGCCAGCAGATTACGGTCATTATGGCCGTTCTTTATACGCATGGCGTGGCG 329 2155846 GCCGTGGGCCGAGCGCCAGTAACGCCAGCAGCGCCAGTATTATACAGAGCGCAGAACAGAGCACAGAACAGAGACAGAACAAACAAAAAA	330 CAGCGCGCCACCTACCGTATCGGTGATGCCTGTGGTGATGCTGTGTGTG	1155786 GCTGCCGGCACCTACCGCATCCACGACGGCGCGCGCGCGC				2155666 GIGGCGGTCAAGAAGAAGTACGCAAGAAGCTCTCATGGCGGAGCTGATTGTTTTCGC 2155607	510 AGGAAACCTACCTGGAAACTATGGCTTTAAAACTTTTGGTTTTGCAGGTGGCAGAGC 569	41555Ub CGGCAACTGGGGGGGGGATCGATGGGCTTCAAGACGTTCGGGTTCGGCTTCGGCGGGT 2155547	570 AGATGTATGGGAGCCTGAAGAAGATGTATACTGGGGAGCGGAAAACCGAATGGCTGGGAGA 629	2155546 CGACCAGTGGGAGCCCGATGAGGTCTATTGGGGCAAGGAAGCCACCAGGCTCGGCTG	630 CAAGCGTATGAAGGTGACGAAGAGTTGAAAATCCCCTGGGAGCGTACAAAAGGGACT 689	2155430	899 CATCTATGTAAACCCGAAGGACCAAGGGCAAGGCCAAGCCCAATCGCTGCTGCGCGCGTG, 749 2155429 GATCTACGTGAACGCGAAGGCCGAACGCGAACCCGAACGCCAATGCCCAAGGCCGAACGCAACGCAACGCAACGCCAACGCCAACGCCAACGCAACACGAACACGAACGCAACGCAACGCAACGCAACACGAACACACAACA	750 TATTCGTGAGACTTTTGGCCGAATGGATGATGAGGAAGAACGTGGCTTCTTATAGC 800	2155369 CATTCGCGGGGCGTGCGCGCATGGCCGTGAACGACGTCGAAACGGCGGGCG	810 GGTGGACACACTTCGGAAAAACCCATGCTGCTGCCGATGCGGGAAATATGTGGGCTG 869		870 AGAGCCTGCCGCAGGTATTGAAGAAATGAGCTGGGGTGGAAAAACACCTACGGCAC 929	2155252 CGAACCCCAGGCTGCTCCGCTGGAGCAGATGGGCTTGGGCTGGAAGAGCTCCTATGGCAC 2155193	930 CGGACACGCTGCGGATACCATCACCAGTGGACTACAAGGCGCCTGGACCAAGACCCCTAC 989	2155192 CGGAACCGCTAAGGACGCGGATCACCAGCGCATCGAGGTCGTATGGAGGACGAACACCCCGAC 2155133		2155132 GAAATGGGACAACAGTTTCCTCGAGATCCTGTACGCTACGAGTGGGGAGTGGAGGACTGACGAAGAG 2155073	1050 TCCAGCIGAGCITATCAGIGGAAACCAAAAGACGGIGCCGGGGCIGGCACCATACCGGA 1109		1110 Techchrearccascanstescacecrecatriatercarancesacetscection 1169	2155012 CCCGTTCGGCGGCCAGGCGCTCCCCGACAATGCTGGCACTGCTGACCTCTCGCTGG 2154956	1170 CHTGGACCTGATACGAAAAATTTCTCGACGGTACTATGAAAACCCTGATGAGTTTGC 1229
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FGAGCGGATCACGCGTCGCTGGCAGCACCCCGAGGAATTGGC 2154896 CGCCAGCAGATGACGGGACCTACCAGGCAAGGATGGC---AG 2154059 AGCATGGTACAAACTGACACACAGAGATATGGGACCAAAGGTGCG 1289 AGTGCCTCAGGAAGACCTCATCTGGCAAGACCCTATACCAGATGT 1349 AGACGANAACGATATTGAAGGCCTAAAAAGCCAAAATCCTGGAATC 1409 CA---GCAACTTGCCAGGGTACTCAAAACACTAGAAGGTATCCA 1586 GAGCTGGTAAGCACGGCATGGGCTTCTGCATCTACTTTTAGAAA 1469 GGTGCCAACGGTGCACGTATACGACTGGCCCCACAAAAAGACTG 1529 GCGCAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGATTGT 1646 GGTGTAGAAAAGCTGCAAAAGATGCTGGCCATGAGGTGCAGGT 1706 CGAGCGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTTCGA 1766 GCTGACGCCTTTAGAAACTACATTAAACCGGAGCATAAAGTATC 1826 STAGACCGGGCGCAGCTTCTGTCGCTTTCGGCACCAGAAATGAC 1886 ATGCGTGTACTGGGCACCAACTACGACGGTTCGCAGCATGGAGT 1946 GCGATGAATCAGACAAAGTTTTTGAAGGCAGAGACTTCAAAAC 2066 GTGGCACCCGGGTAGACCTGATCTTCGGATCCAATTCCGAGCT 2126 TGTACGGCTGTGCAGATTCTGAAGAAAGTTTGTTAAAGATTT 2186 AAGTAATGGACCTGGACCGGTTTGATCTG 2232

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1410 GGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCATCTATTAGAAA 1469
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                                                                                                                                                                                                                990 TCAATGGAGCAATAACTTTTTGAAAACCTCTTTGGTTACGAGGTGGGAGCTTACCAAAAG
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                                                              510 AGGAAACGTAGCTCTGGAAACTATGGCTTTTTGGTTTTGCAGGTGGCAGAGC
                                                                              690 CATCTATGTAAACCCCGAAGGACCCAACGGCAAGCCAGACCCTATCGCTGCTGCGCGTGA
                                                                                                                                                                                                                                                                                                                                              750 CATTCGCGAGACGTTTCGCCGCATGAACGACGTCGAAACAGCGGCGCTGATCGT
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                        570 AGATGTATGGGAGCCTGAAGAAGATGTATACTGGGGAGCAGAAACCGAATGGCTGGGAGA
                                                                                                                                                                                            630 CAAGCGCTATGAAGGTGACCGAGAGCTCGAAAATCCCCTGGGAGCCGTACAAATGGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 TACGTATAACACAAACACTGGCGGAAAATGCCCTTTTACCGGAGGTTCGCTTAAGCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 TAAGAAGCTAGAICTGGCAGCGGTTAAAAAGGACCTGGCAGCGCTAATGACAGATTCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 832.4; DB 1; Length 2235;
Pred. No. 2.7e-247;
0; Mismatches 801; Indels 16;
                             GENERALI INFORMATION:
APPLICANT: Cockerill, Franklin R.
APPLICANT: Kilne, Bruce C.
APPLICANT: Mil., James R.
TITLE OF INVENTION: Detection of Isoniazid Resistant,
TITLE OF INVENTION: OF M. Tuberculosis
NUMBER OF SEQUENCES: 22.
                                                                                                                                                                                                                                                                                   COMPUTER . IN FOR COMPATIBLE
CONTROL IN FOR COMPATIBLE
CONTROL DESCRIPTION RELEASE *1.0, VERSION *1.25
APPLICATION NUMBER: 05/08/418,782
                                                                                                                                                    ADDRESSEE: Schwegman, Lundberg & Woessner STREET: 3500 IDS Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                         150.141051
                                                                                                                                                                                                                                                                                                                                                                                               ATORNEY AGENT INFORMATION:
NAME: VOORSENCT, WEATER D.
REGISTRATION WINBER: 30,440
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
Sequence 1, Application US/08418782
Patent No. 5658733
                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: 612-339-3061
INPORMATION PON SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENCH: 2235 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 63.0
Matches 1389; Conservative
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                        CORRESPONDENCE ADDRESS
ADDRESSEE: Schwegmar
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                     CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-08-418-782-1
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COUNTRY: U
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Best Local (
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                                                                                                                                                                                                                                                                                                                               37.2%; Score 832.4; DB 1;
63.0%; Pred. No. 2.7e-247;
iive 0; Mismatches 801;
                                                            NAME: WORSANER, WARREN D.
REGISTRATON WOMES: 30,440
REFERENCE/DOCKET NUMBER: 150,123USO1
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: 612-339-3061
INFORMATION FOR EQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2225 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENSS: single
                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-228-662-1
                   18-APR-1994
                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 63.0%
Matches 1389; Conservative
                               CLASSIFICATION:
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GGAGGACTTTAACCAGGCGCAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGATTGT 1646
                                                                                    GGAGTCATTCAACTCCGCGGGCGCCGGGAACATCAAAGTGTCCTTCGCCGACCTCGTCGT 1643
                                                                                                                        GCTGGCCGGCTGTGCGGGTGTAGAAAAAGCTGCAAAAGATGCTGGCCATGAGGTGCAGGT 1706
                                                                                                                                              GCCTTTCAACCCGGGACGAGGGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTTCGA 1766
                                                                                                                                                                                                                  1767 AGCACTAGAGCCAGCGGCTGACGGCTTTAGAAACTACATTAAACCGGAGCATAAAGTATC 1826
                                                                                                                                                                                                                                                                                                                                 CGCTGAGGAAATGCTCGTAGACCGGGGGGCACTTCTGTCGGTTTTCGGCACCAGAAATGAC 1886
                                                                                                                                                                                                                                                                                                                                                    TGCTTTGGTAGGCGGTATGCGTGTACTGGGCACCAACTACGACGGTTCGCAGCATGGAGT 1946
                                                                                                                                                                                                                                                                                                                                                                                                                        2007 CACTAAATGGGGAGCCAGCGATGAATCAGACAAAGTTTTTGAAGGCAGAGACTTCAAAAC 2066
                                                                                                                                                                                                                                                                                             1764 CGTGCTGGAGCCCAAGGCAGATGGCTTCCGAAACTACCTCGGAAAGGCCAACCCGTTGCC
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                                                                                                              150 ACGCCAACATTCATCGCTATCGGACCCAAACGACCCGGATTTTGACTATGCCGAAGGTT 209
                                                                                                                                                                                                               210 TAAGAAGCTAGATCTGGCAGCGGTTAAAAAGGACCTGGCAGCGCTAATGACAGATTCACA 269
                                                                                                                                                                                                                                               213 CGCGACCATCGACGTTGACGCCTGACGCGGGACATCGAGGAAAGTGATGACCACCTCGCA 272
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                    30 TACGTATAACACAAAACACTGGGGGAAAATGCCCCTTTTACCGGGAGGTTCGCTTAAGCAAAG 89
                                                 33 TACAGAAACCACCACCGGAGCCGCTAGCAACGGCTGTCCCGTCGTGGGTCATATGAAATA 92
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RESISTANT STRAINS

APPLICANT: COCKERILL, FRANKLIN R.
APPLICANT: KLINE, BRUCE C.
APPLICANT: UHL, JAMES R.
TITLE OF INVENTION: DETECTION OF ISONIALD
TITLE OF INVENTION: OF M. TUBERCULOSIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

GENERAL INFORMATION:

ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A. STREET: 3500 IDS CENTER CITY: MINNEAPOLIS STATE: MINNESOTA

MINNESOTA

COUNTRY:

COMPUTER: IBM "CCCompatible CORPATHO. SYSTEM: PC-TOSANS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APLICATION DAYA. APLICATION NOMBER: DS/08/228,662

Floppy disk

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Page 13

Page 14

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Pred. No. 4.8e-213;
0; Mismatches 842; Indels 28;
                                                                                                                               Resistant Strains
                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE PODES:

COMPUTER IN PER COMPATIBLE
COMPUTER: TENDED COMPATIBLE
SOFTWARE: PALENTER PETERS/NS-DOS
SOFTWARE: PALENTER REABBLE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                               APPLICANT: Kline Bruce C.
APPLICANT: Uhl James C.
TITLE OF INVENTION: Defection of Isoniazid ITLE OF INVENTION: Def. M. Tuberculosis
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                            ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATORNET/GENT INFORMATION:
NAME: Neessner: Mersen: 30,440
REDISTRATION NUMBER: 30,440
REPERRENCE/OFCET NUMBER: 150.141051
FELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHONE: 612-339-3051
                                                              Cockerill, Franklin R.
Sequence 2, Application US/08418782
Patent No. 5658733
GENEAL INFORMATION:
APPLICANT: COCKELIII, Franklin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 612-339-0331
TELEPKX: 612-339-3061
INFORMATION FOR SEQ. DD NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2221 base pairs
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Matches 1335; Conservative
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                              Minneapolis
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MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                            55402
                                                                                                                                                                                                                                                                       STATE: M
COUNTRY:
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                                                                                                                                                                                                                                                                                                                            GACAAGCGCTATGAAGGTGACCGAGAGCTCGAAAATCCCCTGGGAGCCGTACAAATGGGA 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATATICGIGAGACITITGGCCGAAIGGCAAIGAAIGACGAAGAAACCGIGGCICICAIA 807
                                                                                                                                                                                                    513 CGGCAACCGCTGCGCTCGGAATCGATGGGCTTCAAGACGTTCGGGTTCGGCTTCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                            688 CTCATCTATGTAAACCCCGAAGGACCCAACGGCAAGCCAGACCCTATCGCTGCTGCGGT
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450 TTGGCCCATCAAACAAAATACGGTCGAAAAATCTCCTGGGCGGATCTAATGATACTCAC
390
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90 TGCAGGTGGCGGCACCAAAACAGGGATTGGTGGCCCAACATGCTCAACCTCGGCATCTT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 TACAGAAACCACCGGAGCCGCTAGCAACGCCTGTCCCGTCGTCGTCTATGAAATA 92
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                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.3%; Score 721.8; DB 1; Best Local Similarity 60.5%; Pred. No. 4.8e-213; Marches 1335; Conservative 0; Mismatches 842.
                                                                                                                                                                                                                                                   150.1230501
                                                                                     us/08/228,662
   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        REPERBYEÇ/DOCKET HUBBER 150.
TELECOMGUNICATION INVORMATION -
TELEPHONE 1612-339-3061
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE GRAACTERSTICS:
LENGTH: 2221 DASS PAIRS
                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WOESSNER, WARREN D.
REGISTRATION NUMBER: 30,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                 APPLICATION NUMBER: US/OF
FILING DATE: 18-APR-1994
                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-228-662-2
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                                                                             TGGGAAGTAAACAACCTCAGCAACTTGCCAGGGTACTCAAAACACTAGAAGGTATCCAG 1587
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688 CICATCIAIGIAAACCCCGAAGGACCCAACGGCAAGCCAGACCCIAICGCIGCIGCGCGI 747
TTGGCCCATCAAAAAAAAAAGGCTCGAAAAATCTCCTGGCCGGATCTAATGATACTCAC
                                                                                                                                     453 GTGGCCGGTCAAGAAGTACGCCAAGAAGCTCTCATGGGCGGACCTGATTGTTTCGC
                                                                                                                                                                                  510 AGGAAAC--GTAGCTCTGGAAACTATGGGCTTTAAAACTTTTGGTTTTGCAGGTGGCAGA
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                                                                                                                               GENERAL INFORMATION:
APPLICANT: CORRESILL, FRANKLIN R.
APPLICANT: KLINE, BRUCE C.
APPLICANT: UHL, JANES R.
TITLE OF INVENTION: DETECTION OF ISONIAZID RESISTANT STRAINS
TITLE OF INVENTION: OF W. TUBERCULOSIS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.

NUMBER OF SEQUENCES:

STREET: 3500 IDS CENTER CITY: MINNEAPOLIS STATE: MINNESOTA COUNTRY: USA

E: Floppy disk IBM PC compatible

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy C

55402

Sequence 2, Application US/08228662 Patent No. 5688639

RESULT 12 US-08-228-662-2

567 572 627

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1828 GCTGAGGAAATGCTCGTAGACCGGGCGCAGCTTCTGTCGCTTTCGGCACCAGAATGACT 1887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICART: Cocketill, Franklin R.
APLICANT: Kline, Bruce C.
APLICANT: Mill, James R.
TITLE OF INVENTION: Detection of Isoniazid I TITLE OF INVENTION: Of M. Tuberculosis NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: 22
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Patent No. 5922575
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AND STATEMENT ON WOMEN: 4.0.0.1.8 NETERINENCE/COCKET NOWER: 3.0.
TELECOMOTICATION INFORMATION
TELECOMOTICATION OF THE STATEMENT 
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STRANDEDNESS: single
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US-08-852-219-2
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US-08-852-219-2
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1456 GGTAQGAAGGGGGGGGGGCAACGGTGGTGACACGCGCACAAGTGGG 1515
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                                                                                                                                                                          CCCGAACCCGAGGCTCCGCTGGAGCAGATGGGCTTGGGCTGGAAGAGCTCGTATGGC
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1870 GIGCIGGIAGGIGGCCIGCGCGCGCAAACTACAAGCGCITACCGCTGGGGCGTG
1888 GCTTTGGTAGGCGGTATGCGTGTACTGGGCACCAACTACGACGGTTCGCAGCATGGAGTG
                                                                                                                                                                                                                    1948 TITACAAATAAGCCGGGTCAGCTATCCAATGACTTCTTTGTAAACCTGCTAGACCTCAAC
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STREET: 119 No. 5922575th Fourth Street, Ste. 203
CTTP: Minneapolis
STRIE: MN
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WEINTH TTPE: Floppy disk
COMPUTER: LEM PC Compatible
OFFRATING STETCH: PC-TOSANS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
SOFTWARE: PATENTIN DEAT.
APPLICATION NUMBER: DS/08/051,219
FLILE DATE: OFFA-1997
CLASSIFICATION: 435
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Page 18

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  270 GGACTGGTGGCCAGCAGATTACGGTCATTATGGCCCCTTCTTTATACGCATGGCGTGGCA
                                                                   330 CAGCGCCGGCACCTACCGTATCGGTGATGGCCGTGGTGGCGGTGGCTCCGGCTCACAGCG
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                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance TITLE OF INVENTION: in Mycobacterium Tuberculosis CORRESPONDENCES 66 CORRESPONDENCE ADDRESS:
2188 GTGAAGGCCTGGGCCAAAGTAATGGACCTGGACCGGTTTGATCTG 2232
             167 GTCGCTGCGTGGGACAGGTGATGAACCTCGACAGGTTCGACGTG 2211
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                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
APPLICATION NUMBER: 05/08/313,185
FILING DATE: 12-0CT-1994
CLASSIFICATION: 435
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Best Local Similarity 60.3%; Prod. NO. 7.2e-213;
Mcrches 1335; Conservative 0; Mismatches 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02356.0068-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               Sequence 45, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0235
TELECOMUNICATION INFORMATION:
TELECHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                    1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                              APPLICARY: YOUNG, DOUGLS
APPLICARY: ADADG, MAGINE
APPLICARY: TELENII, AMBLIO
APPLICARY: TELENII, AMBLIO
TITLE OF INVENTION: REPLIC IN TITLE OF INVENTION: TO MAGINE
TITLE OF INVENTION: TO MAGINE
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APPLICANT: Cole, Stewart
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20005-3315
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US-08-313-185-45
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COUNTRY:
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TITLE OF INVENTION: RAI
TITLE OF INVENTION: in
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                    Dunner
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                                                                                                                CITY: Wash:
STATE: D.C.
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                                                                                 ADDRESSEE:
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                      TCGGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCATCTACTTTTAGA
                                                                               1468 AACTCTGACAAGCGCGGGGGGGCGTGCACGTATACGACTGGCCCCACAAAAGAC
                                                                                                                                                          3425 GGTAGCGACAAGCGCGGCGGCGCCCAACGGTGGTCGCATCCGCCTGCAGCCACAACTCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4795;
Rapid Detection of Antibiotic Resistance
in Mycobacterium Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                  MEDIUM TYPE: Ploppy disk
COMPOTER: IRB PC COMPALIALIA
COMPATRIS: PER COMPALIALIA
SOCTWARR: PREMEITIR RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.3%; Score 721.8; DB 3; Best Local Similarity 60.5%; Pred. No. 7.2e-213; Matches 1335; Conservative 0; Mismatches 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02356.0068-00000
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                  STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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Sequence 45, Application US/09082614A Patent No. 6124098 GENERAL INFORMATION:

-09-082-614A-45

Heym, Beate Cole, Stewart Young, Douglas Zhang, Ying Honore, Nadine Telenti, Amalio Amalio Bodmer, Thomas

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT

APPLICANT: APPLICANT:

Page 21

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2422 GTGGCCGGTCAAGAAGAAGTACGGCAAGAAGCTCTCATGGGGGGGACCTGATTGTTTCGC 2481	510 AGGAAACGTAGCTCTGGAAACTATGGGCTTTAAAACTTTTGGTTTTGCAGGTGGCAGA 567	568 GCAGATGTATGGGAGCCTGAAGAAGATGTACTGGGGAGCAGAAACCGAATGGCTGGGA 627	2542 CGACCAGTGGGAGACCGATGAGGTCTATTGGGGCAAGGAAGCCACCTGGCTCGGC 2596	628 GACAAGGGCTATGAAGGTGACGGAGAGCTCGAAAATCCCCTGGGAGCGGTACAAAAGGGA 687 2597 GATGACGGTTACAAGGGAAACGAGTGAGAGAAGACCGCGTGGCGGGGGGAGAAGGGG 2653	688 CTCATCTATGTAAACCCCGAAGGACCCAAGGCAAGCCAGACCCTATCGCTGCTGCGCGT 747	748 GATATTCGTGAGACTTTTGGCCGAATGCCAATGAAGAAGAAGAAGCGTGGCTCTCATA 807	2714 GACATTCGCGAGACGTTTCGGCGCATGGCCATGAACGACGTCGAAACAGCGGCGCTGATC 2773	808 GCGGGTGGACACACCTTCGGAAAACCCATGGTGCTGCCGATGCGGAGAAATATGTGGGC 867	868 CGAGAGCTGCCGCAGGTATTGAAGAATGAGCTGGGGTGGAAAAACACCTACGGC 927	2831 CCCGAACCCGAGGCTGCTCCGCTGGAGCAGGTTGGGCTGGAAGAGCTCGTATGGC 2890	928 ACCGGACACGGTGCGGATACCATCACCAGTGGACTAGAAGCGCCTGGACCAAGACCCCT 987	ALCUSANTCASTANTANTANTANTANTANTANTANTANTANTANTANTANT	ACGAAATGGGACAACATTCCTCGAGATCCTGTACGGCTACGAGTGGGGAGCTGAGGAG		3011 AGCCTGCTGGCGCTTGGCAATACACGCCAAGGACGCCGCCGGTGCCGGCACCATCCCG 3070	GATGCACATGATCCCAGGACGCTCCATTTATGCTCACTACGGACCTGGCGCTG	GACCCGTICGCGGGCCCAGGGCGCTCCCCGACGATGCTGGCCACTGACCTCTCGCTG	11bb CGGGTGGATCCTGATAACGAAAAATTCCGAAGGTATTGGAAACCTGATGGATT 1227 	1228 GCAGATGCTTTCGCGAAAGCATGGTACAAACTGACACACAGAGATATGGGACCAAAGGTG 1287	3188 GCCGACGACGTCCGCAAGGCCTGGTACAAGCTGATCCACCGAGACATGGGTCCCGTTGCG 3247	1288 CGCTACCTGGGACCAGAAGTGCCTCAGGAAGACCTCATCTGGCAAGACCCTATACCAGAT 1347	1348 GTAAGCCATCCTCTTGTAGACGAAAACGATATTGAAGGCCTAAAAGCCAAAATCCTGGAA 1407		1408 TGGGACTGACGGTAAGGAGCTGGTAAGCACGGCTTCTGCATCTTTTAGA 1467	3365 TCGGGATTGACTGTCTCACAGCTAGTTTCGACCGCATGGGCGGCGGCGCTCGTCGTTCCGT 3424	1468 AACTCTGACAAGCGCGCGGTGCCAACGGTGCACGTATACGACTGGCCCCACAAAAAGAC 1527	3425 GGTAGCGACAAGGGGGGGGGGGCGAACGGTGGGATCCGCCTGCAGCCCAACTCGGG 3484	1528 TGGGAAGTAAACAACCCTCAGCAACTTGCCAGGGTACTCAAAACACTAGAAGGTATCCAG 1587
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GAGGACTTTAACCAGGGGAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGATTGTG 1647 1648 CTGGCCGGCTGTGCGGGTGTAGAAAAGCTGCAAAAGATGCTGGCCATGAGGTGCAGGGT 1707
3599 CTGGTGCGTGTGTGCGCCACAAAGCGGCACAAAGCGCGCTG 3598
3599 CTGGTGGTGCTGTGCGCCACAAAGCGCGCTGCGCGGTG 3558 1708 CCTTTCAACCCGGGACGAGGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTTCGAA 1757 1768 GCACTAGAGCCAGCGGCTGACGCCTTTAGAAACTACATTAAACCGGAGCATAAAGTATCC 1827 3778 1887 1888 GCTTTGGTAGGCGGTATGCGTGTACTGGGCACCAACTACGACGTTCGCAGCATGGAGTG 1947 3898 1948 TITACAAATAAGCCGGGTCAGCTATCCAATGACTTCTTTGTAAACCTGCTAGACCTCAAC 2007 2067 4015 2068 GGCGAAGTAAAGTGGGAGTGGCACCCGGGTAGACCTGATCTTCGGATCCAATTCCGAGCTA 2127 2128 AGAGCCCTCGCAGAAGTGTACGGCTGTGCAGATTCTGAAGAAAGTTTGTTAAAGATTTT 2187 1839 GIGCTGGTAGGTGGCCTGGGGGGTGCTGGGCAAACTACAAAGGCTTACGGTGGGGGTG 2008 ACTAAATGGCGAGCCAGCGATGAATCAGACAAAGTTTTTGAAGGCAGAGACTTCAAAACT 1828 GCTGAGGAAATGCTCGTAGACCGGGCGCAGCTTCTGTCGCTTTCGGCACCAGAAATGACT 3959 ATCACCTGGGAGCCCTCGCCAGCAGATGACGGGACCTACCAGGGCAAGGATGGC---AGT à a à ģ δ ď ď a ò g ŏ 9 à g à Q à à

Search completed: October 8, 2003, 15:34:05 Job time : 137.323 secs THIS PAGE BLANK (USPTO)

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

8, 2003, 12:53:54 ; Search time 572.431 Seconds (without alignments) 10144.788 Million cell updates/sec October Run on:

US-09-884-889-7

1 atggaaaatcacaaacactc.....accggtttgatctgaaataa 2238 Perfect score: Scoring table: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0.

Total number of hits satisfying chosen parameters:

1731049 seqs, 1297405648 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first. 45 summaries

Published\_Applications\_NA:\* Database :

/cgn2\_6/ptcodata/2/pubpna/US09\_NEW\_PUB.seg:\*/cgn2\_6/ptcodata/2/pubpna/US10A\_PUBCOMB.seg:\*/cgn2\_6/ptcodata/2/pubpna/US10B\_PUBCOMB.seg:\* /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seg:\* /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRANS

			œ			SUMMARIES		
Result No.	ult No.	Score	Query	Query Match Length DB	80	91	Description	
	٦	2238	100.0	_	10	US-09-884-889-7	Sequence 7, Appli	
o	7	844.4	37.7	80	15	US-10-080-170-645	Sequence 645, App	
	m	672.2	30.0	_	10	US-09-884-889-5	Sequence 5, Appli	
	4	251.8	11.3	620	11	US-09-940-925A-145	145	
U	Ŋ	251.8	11.3	620	11	US-09-940-925A-149	Sequence 149, App	
	9	251.8	11.3	1 620	11	US-09-941-193A-145	Sequence 145, App	
υ	7	251.8.	11.3	620	11	US-09-941-193A-149	149, 2	
	œ	250.2	11.2		11	US-09-940-925A-143	Sequence 143, App	
	σ	250.2	11.2	620	1	US-09-940-925A-146	146,	
υ	10	250.2	11.2		11	US-09-940-925A-147	147,	
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	12	250.2	11.2		11	US-09-941-193A-143	143,	
	13	250.2	11.2	8 620	1	US-09-941-193A-146	146,	
U	14	250.2	11.2		:	US-09-941-193A-147	Sequence 147, App	
Ų	12	250.2	11.2		11	US-09-941-193A-150	Sequence 150, App	
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-046	41-	41-	825-574-1	382-	325-	325-	382-	382-	325-	382-	-, 11	502	-156	140-	4	42	128-	133-	146-	31-9	184	184	801	-72	10-140-472-54	5	142	158-790-54
JS-09-940-925A-1	JS-09-941-193A-144	JS-09-941-193A-1	3-60-SC	JS-09-882-945A-	3-60	US-09-825-574-	JS-09-882-945A	US-09-882-945A-	3-60	3-60	US-09-917-800A-1	US-10-205-194-1	US-10-156-761-1	US-10-140-472-358	US-10-141-761-358	10-1	-01	10-1	-01	8-78	10-1	-01	-01	10-(	10-1	10-1	10-1	US-10-3
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ALIGNMENTS

APPLICANT: DIVERSA CORPORATION
APPLICANT: NOBERFOON Dan
APPLICANT: APAHTKAL! INdrall:
APPLICANT: ANHIKAL! ROBERT
TITLE OF INVENTION: CATALAGES
FILLE REFERENCE: DIVENTION CURRENT FILLOW DATE: 3001-06-19
PRIOR PELLOK DATE: 1999-10-05
PRIOR PELLING DATE: 1999-10-05 PRIOR APPLICATION NUMBER: US 08/951,844
PRIOR FILING DATE: 1997-10-16
PRIOR APPLICATION NUMBER: US 08/674,887
PRIOR FILING DATE: 1996-07-03 Sequence 7, Application US/09884889 Patent No. US20020102680Al SOFTWARE: Patentin version 3.0 SEQ ID NO 7 SEQ ID NOS: 8 GENERAL INFORMATION: LENGTH: 2238 US-09-884-889-7 NUMBER OF

DB 10; Length 2238; 100.0%; Score 2238; 100.0%; Pred. No. 0; Live 0; Mismatches ORGANISM: Microscilla furvescens US-09-884-889-7 Query Match
Best Local Similarity 100.0
Matches 2238; Conservative

DNA

ö 1 ATGGAAAATCACAAACACTCAGGATCTTCTACGTATAACACAAACACTGGGGGAAAATGC 60 1 ATGGAAAATCACAAACACTCAGGATCTTCTACGTATAACACAAAACTGGCGGAAAATGC 60 0; Gaps Indels ö à 윰 ð g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 645. Application US/10080170
| Publication No. US20030129601A1
| CENTEAL INFORMATION NO. US20030129601A1
| APPLICANT OCLE, S.T.
| TILL OF INVENTION: INDEXIVEN ARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TILLE REPRENCE: 03495.027
| TILL OF INVENTION: INDEXIVEN OF WICOBACTERIOSES
| TILLE REPRENCE: 03495.027
| CHURRAY APPLICATION NUMBER: US/10/090,170
| PRIOR PRILICATION NUMBER: 05/10/090,170
| PRIOR PRILICATION NUMBER: 60/270,123
| PRIOR PRICICATION NUMBER: 60/270,123
| PRIOR PRILICATION PATE: 2001-05-22
| SOFTWANT: AFFARCH VET. 2.2
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                                                                                                                                                                                                                                                                                                                                                                                            210 TAAGAAGCTAGATCTGGCAGCGGTTAAAAAGGACCTGGCAGCGCTAATGACAGATTCACA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCGCCGCCACCTACCGTATCGGTGATGGCCGTGGTGGCGGGTGGCTCCGGCTCACAGCG 389
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                                                                                                                                                                                                                          Length 82993;
                                                                                                                                                                                                                       Score 844.4; DB 15; Length
Pred. No. 8.4e-265;
0; Mismatches 801; Indels
                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-645
                                                                                                                                                                                                                       37.7%;
illarity 63.0%;
Conservative
                                                                                                                                                                                                                                 Similarity
US-10-080-170-645/c
                                                                                                                                                         SEQ ID NO 645
LENGTH: 82993
                                                                                                                                                                                                                                 Best Local Sim:
Matches 1390;
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39522 39462 GCCCTTCACCCCGGGCCGCACGCATGCGTCGCAGGAACAACCGACGTGGAATCCTTTGC 38745 39642 1049 AGCACTAGAGCCAGCGGCTGACGCTTTAGAAACTACATTAAACCGGAGCATAAAGTATC 1826 1827 CGCTGAGGAAATGCTCGTAGACCGGGCGCAGCTTCTGTCGCTTTCGGCACCAGAATGAC 1886 989 809 38984 GGAGGICAACGACCCGACGGGATCIGCGCAAGGICAITCGCACCCIGGAAGAGAICCA 1530 GGAAGTAAACAACCCTCA---GCAACTTGCCAGGGTACTCAAAACACTAGAAGGTATCCA GCCTTTCAACCCGGGACGAGCGGATGCCACCGCTGAGCAAACCGATGTGGAAGCTTTCGA CGGAACCGGTAAGGACGCGATCACCAGCGGCATCGAGGTCGTATGGACGACGACCGGAC 1230 AGATGCTTTCGCGAAAGCAFGGTACAAACTGACACACAGAGATATGGGACCAAAGGTGCG 1350 AAGCCATCCTCTTGTAGACGAAAACGATATTGAAGGCCTAAAAGCCAAAATCCTGGAATC 1410 GGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCATCTACTTTAGAAA 1470 CTCTGACAAGCGCGGCGGTGCCAACGGTGCACGTATACGACTGGCCCCACAAAAGACTG GGAGGACTTTAACCAGGCGCAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGATTGT GCTGGCCGGCTGTGCGGGTGTAGAAAGCTGCAAAAGATGCTGGCCATGAGGTGCAGGT CGTGCTGGAGCCCAAGGCAGATGGCTTCCGAAACTACCTCGGAAAGGGCAACCCGTTGCC AGAGCCTGCCGCCGCGGGTATTGAAGAAATGAGCCTGGGGTGGAAAAACACCTACGGCAC 39641 CGAACCCGAGGCTGCTCCGCTGGAGCAGATGGGCTTGGGCTGGAAGAGCTCGTATGGCAC TCAATGGAGCAATAACTTTTTTGAAAACCTCTTTGGTTACGAGTGGGAGCTTACCAAAAG 1050 TCCAGCTGGAGCTTATCAGTGGAAACCAAAAGACGGTGCCGGGGCTGGCACCATACCGGA CATGGACCCTGATTACGAAAAATTTCTCGACGGTACTATGAAAACCCTGATGAGTTTGC 38924 GGAGTCATTCAACTCCGCGGCGCGGGAACATCAAAGTGTCCTTCGCCGACCTCGTCGT 38864 GCTCGGTGGCTGTGCCGCCATAGAGAAAGCAGCAAAGGCGGCTGGCCACAACATCACGGT 750 TATTCGTGAGACTTTTGGCCGAATGGCAATGACGAAGAAACCGTGGCTCTCATAGC GGGTGGACACATCGGAAAAACCCATGGTGCTGCCGATCCGGAGAAATATGTGGGCCCG CGGACACGGGTGCGGATACCATCACCAGTGGACTAGAAGGCGCCTGGACCAAGACCCCTAC TGCACATGATCCCAGCAAGTCGCACGCTCCATTTATGCTCACTACGGACCTGGCGCTGCG 1290 CTACCTGGGACCAGAAGTGCCTCAGGAAGACCTCATCTGGCAAGACCTATACCAGATGT

339 GCCGGCTGACTGGGGGCACTACGGGGGTTGCATGGCCTGTGGCCCTGGGGGGGG	1347 ATCACGTTACATCGGCCCGGAAGTGCCGGCAGAAGACCTGATTTGGCAAGACCCGATTCC 1406 1344 AGATGTAAGCCATCCTTGTAGACGAAAACGATATTGAAGGCCTAAAAGCCAAAATCCT 1403 14
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	do yo
1986   10   11   11   11   11   11   11   1	Db 270 CGATTCCACGCCTGAAGAAGATCTCCACGCGTTGATGCCAAGAGTGGTG 329  Qy 279 GCCAGCAGATTATGGCCCCTTCTTTATACGCTTGGCTGCACACGCCGG 338

Fri Oct 10 11:39:17 2003

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1156 GACCTGGCGCTGCGCATGGACCCTGATTACGAAAAATTTCTCGACGGTACTATGAAAAC 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 620;
                                                                              MEDIUM TYPE: Floppy disk
COMPUTES: IRM PC Compatible.
COMPUTES: TRM PC COMPATIBLE.DOS
SOUTHWARE: PAREITIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,925A
FILIME DATE: 10.5Un-2002
CLASSIFICATION: <a href="https://documents.com/">documents/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 251.8; DB 1.
Pred. No. 1.6e-71;
                                                                                                                                                                                                                                                ATTORNEY, AGREY INVOKATION

NAME: CARROLL, PETER 6.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: PORS-01756

FELECOMMUNICATION INFORMATION:
STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%;
                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.9
Matches 398; Conservative
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                                           1464 TAGAAACTCTGACAAGCGCGGCGGTGCCAACGGTGCACGTATACGACTGGCCCCACAAAA 1523
                                                                                                                                                                                   1524 AGACTGGGAAGTAAACAACCCTCAGCAACTTGCCAGGGTACTCAAAACACTAGAAGGTAT 1583
                                                                                                                                                                                                                                                                    CCAGGAGGACTTTAACCAGGCGCAATCAGATAACAAAGCAGTATCGTTGGCCGACCTGAT 1643
                                                                                                                                                                                                                                                                                                             -----GAGCGTCTACGAGCAGATCTCTGCCGACACGCGCGCTAGCATCGCGGACGTGAT 1670
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                 GGAATCGGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCATCTACTTT 1463
                                                                                                                            2031 GGGGAACAGCTGG-----AAGCCGGTAGGTAGCAACGCCTACGAAATCCGCGACCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1085 GACCGGTGCCGTGAAGTGGACCGCCTCGCGGGTGGATCTGGTATTTGGTTCCAACTCGCT
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TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 145, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 165
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1456 TCTACTTTTAGAAACTCTGACAAGCGCGGCGGTGCCAACGGTGCACGTATACGACTGGCC 1515
                                                                                           1276 GGACCAAAGGTGCGCTACCTGGGACCAGAAGTGCCTCAGGAAGACCTCATCTGGCAAGAC 1335
                                                                                                                                                                                                                                                                      1396 AAAATCCTGGAATCGGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCA 1455
      1336 CCTATACCAGATGTAAGCCATCCTCTTGTAGACGAAAACGATATTGAAGGCCTAAAAGCC 1395
                                                                                                                   323 CCCGAGGAATTGGCCGACGAGTTCGCCAAGGCCTGGTACAAGCTGATCCACCGAGACATG
                                                                                                                                                                                                         203 CCGGTCCCTGCGGTCAGCCACCTCGTCGGCGAAGCCGAGATTGCCAGCCTTAAGAGC
                                                                                                                                                                                                                                                                                                 83 TCGTCGTTCCGTGGTAGCGACAAGCGCGGCGCCCAACGGTGGTCGCATCCGCCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: INH PC Compatible
OVERATING SISTEM: PC-DOS/MS-DOS
SOFTWARR: PRETENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.3%; Score 251.8; DB 11;
63.9%; Pred. No. 1.6e-71;
tive 0; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER 6.
REGISTRATION NUMBER: 32,837
REPERENCE/DOCKET NUMBER: FORS-01756
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/941,193A FILING DATE: 28-Aug-2001 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
COMPUTER REALABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
                                                                                                                                                                                                                                                                                                                                                                                                                                             1516 CCACAAAAGACTGGGAAGTAAA 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-941-193A-145; Application US/09941193A; Sequence 145, Application US/09941193A; Publication No. US20030108873A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL INFORMATION:
APPLICANT: BROW, MARY ANN D.
TYAMICHEV, VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 CCACAAGTCGGGTGGGAGGTCAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHOGENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : SAN FRANCISCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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Best Local Similarity 63.9%;
Matches 398; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1036 GAGCTTACCAAAAGTCCAGGTGGAGCTTATCAGTGGAAACCAAAAGACGGTGCCGGGGCT 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1096 GGCACCATACCGGATGCACATGATCCCAGCAAGTCGCACGCTCCATTATGCTCACTACG 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACCTGGCGCTGCCCATGGACCCTGATTACGAAAAATTTCTCGACGGTACTATGAAAAC 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       916 AACACCTACGGCACCGGACACGGTGCGGATACCATCACCAGTGGACTAGAAGGCGCCTGG 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620 AGCTCGTATGCCACCGGAACCGGTAAGGACGCGATCACCAGCGGCATCGAGGTCGTATGG 561
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                                                                                                                                                                                                                                    LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAZID DETECTION AND IDENTIFICATION OF PATHOGENS
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COMPUTER: THE P. C. COMPATIBLE
SOFTHARE: PATENTIN FOLDOS/AS-DOS
SOFTHARE: PATENTIN DARM:
APPLICATION NUMBER: US/09/940,925A
FILIAND DARE: 1-U-Un-1200-700
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES, 165
CORRESPONDENCE ADDRESS:
ADDRESSEE, WEDLEN & CARROLL
STREET, 220 MONFORMY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 251.8; DB 11;
Pred. No. 1.6e-71;
0; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: CAROLI, PETE R.
REGISTRATION NUMBER: 32,837
REPERNICE/POETE INVAMER: FORS-01756
TELEORMICATION INFORMATION:
TELEPRONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 149:
   1516 CCACAAAAGACTGGGAAGTAAA 1538
                     598 CCACAAGTCGGGTGGGAGGTCAA 620
                                                                                                                                                     Sequence 149, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.3%;
Best Local Similarity 63.9%;
Matches 398; Conservative 0
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OLIVE, DAVID M.
                        Sequence 149, Application US/09941193A Publication No. US20030108873A1 GENERAL INFORMATION:
US-09-941-193A-149/C
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1456 TCTACTTTTAGAAACTCTGACAAGGGGGGGGGGGGCAAGGGTGCACGTATACGACTGGGC 1515
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      61 ACGAACACCCGGACGAAATGGGACAACAGTTTCCTCGAGATTCCTGTACGGCTACGAGTGG 120
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TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE PORM:
COMPUTER READABLE PORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM FC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
OFFWENT APPLICATION DATA:
FILING DATE: 10-Jun-2002
CLASSIFICATION NUMBER: US/09/940,925A
CLASSIFICATION: CORROWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223; Indels
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ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 250.2; DB 11; 63.7%; Pred. No. 5.4e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: FORS-01756 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 146:
                                                                                                                                                                1516 CCACAAAAGACTGGGAAGTAAA 1538
                                                                                                                                                                                             598 CCACAAGTCGGGTGGGAGGTCAA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                       Sequence 146, Application US/09940925A; Publication No. US20030054338A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 705-64:
TELEFAX: (415) 397-6336
INFORMATION FOR SEQ ID NO: 146:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 620 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparitible
COMPUTER: IBM PC Comparitible
COMPUTER: IBM PC COMPARITIBLE
SOCTHANER: PARENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,925A
CILASSIFICATION COMPARITIBLE SOCIATION: CONTROWN
                                                                                 ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 223;
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Pred. No. 5.4e-71
                                                                                                                                                                             COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 143:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 620 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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                                               NUMBER OF SEQUENCES: 165
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                       STATE: CALIFORNIA
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                                                                                                                                                                                                                                                     .036 GAGCTTACCAAAAGTCCAGCTGGAGCTTATCAGTGGAAACCAAAAGACGGTGCCGGGCT
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                                                                                                            Gaps
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                                                                     Length 620;
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LYANGERY, YLCYOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                          Indels
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ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                     DB 11;
                                                                  Score 250.2; DB 11;
Pred. No. 5.4e-71;
0; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UNITED STATES OF AMERICA 2IP: 94104
; SEQUENCE DESCRIPTION: SEQ ID NO: 147: US-09-940-925A-147
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COMPUTER: IBM PC compatible
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STATE: CALIFORNIA
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                                                                J1.2%;
Best Local Similarity 63.7%;
Matches 397; Conservative
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        181 GGCACCATCGACCGGATCG---GCGGGCCAGGGGGGCGCTCCCGACGATGGTGGCCACT 237
                                                                                                    358 GGTCCCGTTGCGAGATACCTTGGGCCGCTGGTCCCCAAGCAGCCTGCTGTGGCAGGAT 417
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LVANGERY, YTCROR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIADLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORREY, CAGENT ITOROGENATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 12,837
REPERRENCE/DOCKET NUMBER: PORS-01756
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/940,925A FILING DATE: 10-Jun-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1516 CCACAAAAGACTGGGAAGTAAA 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              598 CCACAAGTCGGGTGGGAGGTCAA 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 147, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 147:
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECTION CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
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976 ACCAAGACCCCTACTCAATGGAGCAATAACTTTTTTGAAAACCTCTTTGGTTACGAGTGG 1035
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OLIVUE, DAVID M.
TITLE OF INVENTION: RAID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 620;
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READMILE PORPH (1848)

CMADUTH THEE: PLORPH clask
CMADUTH THEE: PLORPH clask
CMADUTER: THE PC-DOSABLABLE
COMPARIE: STATEMEN PC-DOSABLABLE
CURRENT APPLICATION NUMBER: US/09/91,193A
FILING NAME: CARROLL, PERER C.
CLASSIFICATION NUMBER: US/09/91,193A
ATTORNEY AGRET INFONANTION:
NAME: CARROLL, PERER C.
RECISTRATION NUMBER: 3, 837
REPRENENCE, POCKET NUMBER: 9. 803-01756
TELECOMMUNICATION INFORMATION:
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Pred. No. 5.4e-71;
0; Mismatches 223; Indels
                                                                                                                                                                                                                                                        ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                              COUNTRY: UNITED STATES OF AMERICA 21P: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 143:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 143:
                                                                                                                                                                                      PATHOGENS
                                                                                                APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 620 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                           Sequence 143, Application US/09:
Publication No. US20030108873A1
GENERAL INFORMATION:
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.2%;
Best Local Similarity 63.7%;
Matches 397; Conservative
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  !OPOLOGY: linear
      US-09-941-193A-143
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                     : PatentIn Release #1.0, Version #1.30
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63.7%; Pred. No. 5.4e-71;
tive 0; Mismatches 223;
                                                                                                                            ATTORNEY CHEMPATON;

NAME: CARROLL, PETER C.

REGISTRATION NUMBR: 20,837

REFERENCE/POCKET NUMBR: FORS-01756

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEX 10,150

SEXOURNE CHARACTERISTICS:
                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-09-940-925a-150
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 63.73
Matches 397; Conservative
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1156 GACCTGGCGCTGCGCATGGACCCTGATTACGAAAAATTTCTCGACGGTACTATGAAAAC 1215
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                                                                                                                       61 ACGAACACCCCGACGAAATGGGACAACAGTTTCCTCGAGATCCTGTACGGCTACGAGTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                        418 CCGGTCCCTGCGGTCAGCCACGACCTCGTCGGCGAAGCCGAGATTGCCAGCCTTAAGAGC
                                                                          1036 GAGCTTACCAAAAGTCCAGCTGGAGCTTATCAGTGGAAACCAAAAGACGGTGCCGGGGCT
                                                                                                                                                                                                                                                                                      181 GGCACCATCCCGGACCCGTTCG---GCGGGCCCAGGGCGCTCCCCGACGATGCTGGCCACT
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TITLE OF INVENTION: RAID DETECTION AND IDENTIFICATION OF PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/941,193A FILING DATE: 28-Aug-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UNITED STATES OF AMERICA
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ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598 CCACAAGTCGGGTGGGAGGTCAA 620
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: (415) 397-8338
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STATE: CALIFORNIA
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US-09-941-193A-147/c
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                                                                     1336 CCTATACCAGATGTAAGCCATCCTCTTGTAGACGAAAACGATATTGAAGGCCTAAAAGCC 1395
                                                                                                                                                                                                           1396 AAAATCCTGGAATCGGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCA 1455
358 GGTCCCGTTGCGAGATACCTTGGGCCGCTGGTCCCCAAGCAGCACCCTGCTGTGGCAGGAT 417
                                                                                                                  1 AGCTCGTAIGGCACCGGAACCGGTAAGGACGCGAICACCACCGCCAICGAGGICGTAIGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MAS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
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REDISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
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APPLICATION NUBER: US/09/941,193A
FILLIG DATE: 2001
CLASSIFICATION: <a href="checkbase">CLASSIFICATION: <a href="checkbase">CLASSIFICATION: <a href="checkbase">CGASSIFICATION: <a href=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 146:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: SAN FRANCISCO
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COMPUTER IN TO COMPATIBLE
SOFTWARE: PACIFORM OF SAFETY
SOFTWARE: PACIFORM DATA:
APPLICATION NUMBER: US/09/941,193A
FILIANTON NUMBER: US/09/941,193A
CLASSIFICATION: CURMONNO
                                                                                                                                                                                                                                                         ATTORNEY/ACENT INFORMATION
NAME: ACREOLE PETR G.
RAGISTARION NUMBER: 3, 837
REPREDENCE/ACENT NUMBER: 908-01756
TELECOMMINICATION INFORMATION:
TELECOM (18, 13) 397-838
INFORMATION POSSILION: 8200ENCE CHARACTERISTICS:
                                              COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 150: US-09-941-1334-150
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                             CALIFORNIA
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                                                                                                                                                                                                   DB 11; Length 620;
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OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                             Score 250.2; DB 11; Length
Pred. No. 5.4e-71;
0; Mismatches 223; Indels
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STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 147:
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                SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: 147;
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   datches 397; Conservative
                                                                                                                                                                                                                   Similarity
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Search completed: October 8, 2003, 19:55:28 Job time : 577.431 secs

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AW179968 BQ752115 BQ751801 BU065388

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BMB6570 F BQ751114 BQ751114 BQ751114 BQ751114 BQ751114 BQ761114 BQ761114 BQ761118 BQ76118 BQ76118 BQ76118 BQ75118 BQ75

Run on:

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BH403595 786 bp DNA linear GSS 11-DEC-2001
AG-ND-127D17.TF ND-TAM Anopheles gambiae genomic clone AG-ND-127D17
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Hong V. S. Hogen J. R. Wang, X., Sarkar, A., Sim, C., Loftus, B.J., Re
A.C., Miff, B. R., Certillo, J.L., Black, K., Zhang, H.-B., Gardner, M.J.
and Colling? E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Construction of a BAC library and generation of BAC end construction of a Sac ender sequencing of the African malaria mosquito Anophales gambiae
MAC. Gener. Genomics 268 (6), 720-728 (2003)
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
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Contect: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                      , genomic survey sequence.
BH403595
BH403595.1 GI:17349811
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BH403595/c
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MEDLINE
PUBMED
COMMENT
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
 BH403595 AG-ND-127
AF075865 AF075865
CD377714 PTWM02883
BH401331 AG-ND-137
                                                     ; Search time 4638.63 Seconds
(without alignments)
11726.187 Million cell updates/sec
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scree greater than or equal to the scree of the result being printed,
and is derived by analysis of the total score distribution.
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       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                           22781392 segs, 12152238056 residues
                                                                                                                                                          Fotal number of hits satisfying chosen parameters:
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                                                     October 8, 2003, 07:49:13;
                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH403595
AF075865
CD377714
BH401331
                                                                                                                           Gapop 10.0 , Gapext 1.0
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Match Length
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                                                                                             Perfect score:
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Result

ALIGNMENTS

AW180906 BE758793 CD457487

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#4075865 almonella typhimurium Liz. Lambda DSRI II Salmonella typhimurium Liz. Lambda DSRI II Salmonella typhimurium penomic clone 1079-77, genomic eurvey sequence.
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Salmonella typhimurium
Bacteria; Protebbecteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceas; Salmonella.
I (bases 1 to 1018)
Nong N. M. "t. Wong K. K. Enson, N. R. and McClelland, M.
Sample sequencing of a Salmonella typhimurium Lrz lambda library;
Sample sequencing of a Salmonella typhimurium Lrz lambda library;
Exes Maircoblol. Lett. 173 (2), 411-423 (1999)
      137 TTATTCCGAATGCTTTTGATGCAGAGAAAAAGGTCCGGCTTATATGCTTACAACTGACC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DASH II"
Li-Cor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 GCGCGTTACATCGGACCGGAAGTGCCGAAAGAAGAGTCTGATCTGGCAGGACCCGTTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1345 GATGTAAGCCATCCTCTTGTAGACGAAAACGATATTGAAGGCCTAAAAGCCAAAATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 CAACCGCTCTATCAGCCAACGCAGGAAGACATTATCAA----CCTGAAAGCGGCGATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1405 GAATCGGGACTGACGGTAAGCGAGCTGGTAAGCACGGCATGGGCTTCTGCATCTACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 GCATCGGGGCTTCTATTAGCGAGATGGTTTCGGTTGCCTGGGCATCCGCGTCTACTTTC
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DASH II; sequenced using
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/mol_type-"genomic DNA"
/strain-"LT2"
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Pred. No. 1.2e-71;
0; Mismatches 389;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Biology
Sidney Klamel Cancer Center
3099 Science Park Road, San Diego,
Email: mcclelland@lifscl.sdsu.edu
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/note="Vector: Lambda D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:602"
/clone="1079-T7"
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                                                                                                                                    1220 ATGAGTTTGCAGATGCT 1236
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                                                                                                                                                            Contact: McClelland M
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il Similarity 58.6%;
595; Conservative
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278 c
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                                                                                                                                                                                                                                             RESULT 2
AF075865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               980 AGACCCCTACTCAATGGAGCAATAACTTTTTGAAAACCTCTTTGGTTACGAGTGGGAGC 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1040 TTACCAAAAGTCCAGCTGGAGCTTATCAGTGGAAACCAAAAGACGGTGCCGGGGCTGGCA 1099
                                                                              mis close is from an Agambiae BAC library (ND-TAM) provided by F.H. Colliss and sequenced by The Institute for Genomic Research TGRR). The BAC library was generated from A. gambiae PEST strain DNA. Na Setzecked from Anoly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from microorganisms that inhabit library was constructed at Texas AAM University, College Station, Texas AAM University, College Station, Texas AAM University, Solider Station, Texas T7843-2123, USA using a Hindili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 CTCACAGGAAACGTAGCTCTGGAAACTATGGGCTTTAAAAACTTTTGGT-TTTGCAGGTGG 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 ATCTGGGCCGAGAGCCTGCCGCCGCAGTATTGAAGAAATGAGCCTGGGGTGGAAAAAAA 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 --GTAGGAGCTGAGGCTCCGGAATTGAAGCTCAGGGATTAGGTTGGGCAAGTA 312
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      USA
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Center Dr., Rockville, MD 20850, 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 13.2%; Score 296.2; DB 28; Il Similarity 66.5%; Pred. No. 1.2e-75; 490; Conservative 0; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                   /organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:7165"
/clone="AG-ND-127D17"
/clone_lib="ND-TAN"
/note="Vector: pbCBAC1; Si
a 211 c 148 g 244
                                                                                                                                                                                                                                                                                                                               Location/Qualiflers
   9712 Medical Center Dr.,
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
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Class: BAC ends.
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Email: chrisealpha.szn.it Diatom EST Database(http://avesthagen.sznbowler.com) Seg primer: T3 Dackward POLYA-Ves. Location(Jullifers 1. 870 ACTA LEW Phaeodactylum tricornutum" ACL-Type-"RNN" ACL-Type-"RNN" ACL-Type-"RNN" ACTA RIFF: LEXAON: 2850 ACTOR Line-"Corpessor ACTOR LINE-"CORPESS	Ouery Match 12.0%; Score 269; DB 14; Length 873; Best Local Similarity 60.3%; Pred. No.1.4e-67; Matches 476; Conservative 0, Mismatches 309; Indels 4; Gaps Matches 1454 CATCACTACTACAACACTCGACAAGGGGGGCAAAGGGGGGCCAAAGGGGAAAGGGGGAAAGGGGAAAGGGGAAAGGGGAAAGGGG	1514   COCCOADANAAGACTGGGAAGTAAGAAGCTGAGAGAGTGTGCADAAGAC 1573	181 TAGGAGTTTGATGTTCTAGGGGTTGCGCCGCAATTGAGTTGCTGCAAAAAGCTG  1691 GCATGAGGTGCGTTCTAGGTGGTTGCTGCAATTGAGTTGCTGCAAAAAAGCTG  1691 GCATGAGGTGCGTTCTAGGTGCCGCGCAACGGAGGCGAAGCCGAAGCGAACGAA	Db 301 TTGCAGAATCATTTGACGCAGCAGCAGCAGAGGCTTTCGCAACTATTTGAAAG 360  Qy 1811 CGGAGCATAAAGTATCGCTGAGGAAATGCTCGTAGACGGGGGGGAGCTTCTGTCGCTTT 1870  Db 361 AGGCCCAACCACAAAGGGAAGGCTCTGTTTATTTTTTTTT	1911 CONTROLLE C
1525 GACTGGGAAGTAAACCACCTCAGCAACTTGCCAGGGTACTCAAAACACTAGAAGGTATT 1584	GAAGCACTAGAGCCAGCGGCTGACGGCTTAGAAACTACATTAAACCGGAGCATAAAGTA TCGCTGCTTGAGCATTAGATGCTGATGGGTTGCTTGTGGTGTGTGT	1885 648 1945 707 2005	767 2065 827 2125	Db 887 CTGCGCGCGCTGGCGGAAGTTACGCGACTGTAGCGAAGTTGCGAAGAAGA 946  Qy 2184 TTTTGTGAAGGCCTGGCCCAAAGTAATGGACCTGGACGGTTTGATCTGAAATA 2238	CD377714 CD3

Cy 1418 CGGTAAGCAGGGATGGGCTTCTGCATCTTGTAAAACTCTGACA 1477	181   CANTITICTGAACTGGTATCTRAGGATGGCTTTTTAATTCCGAGGATGGGTT 240     1478   AGGGGGGGGGGTGCAACGATGGCTTTTAATTCCGAGGATGGGTT 240     1478   AGGGGGGGGGGCAACGGTGCACGATAGGCTTGGCCCAAAAAAGTTGGATGAATAGTAAAAGAGTTGGGGGGTAA 300     1538   AGAACCGTCAAGCAACTTGCAGGATGAACACTTGGTATCGAACACTAGAAGAGTTA 1597     11   1   1   1   1   1   1   1   1	1658   GTGCGGGTCTAGANAAGCTGCANAGATGCTGGCCATGAGGTGCCAGGGGCGGGGGGGGGG	RESULT 5  AN17966 AN17967 AN17966 AN17967 AN17966 AN17967 AN17	FEAT: +44(0)1275 394281  EMALI: John.AntgraswaseBabrc.ac.uk Insert.LengtraswaseBabrc.ac.uk Insert.Length: 2600 Std Error: 0.00  Seq prime: M3 roverse.  L. 729.  A. 720.  A. 7	/clone_lba_wgAA0202. /clone_lba_wgAA0202. /clone_lba_wgAA0202. /clone_lba_wgAA0202. /note="Vector: psPoRT]: Library constructed from cultures utilizing ammonium lons as a source of nitrogen" ORIGIN  OBEGIN  11.6%; Score 259.8; DB 9; Length 729;
Db 781 TTGAAAANA 789	RESULT 4 BH401331 LCCUS BH401331 LCCUS BH401331 LCCUS DEFINITION AG-TD-127N19.TR.1 ND-TAM Anopheles gamblae genomic clone AC-TD-137N15, genomic survey sequence. VERSION H401331.1 G:17347547 SOURCE Anopheles gamblae (African malaria mosquito) SOURCE ORGANISM Anopheles gamblae (African malaria mosquito) RETWOODS SOURCE Anopheles gamblae (African malaria mosquito) RETWOODS SOURCE Anopheles gamblae (African malaria mosquito) RETWOODS SOURCE ANOPHEROSOS, Althropoda; Hexapoda; Insecta; Pterryota; ROPPEROSOS SINDADEROSOS, Althropoda; Hexapoda; Insecta; Pterryota;	ADDRESS. AUTHORS Host, X.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., Ren AUTHORS Host, X.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., Ren And Collins, F. R. Carlile, J.L., Black, K., Zhang, HB., Gardner, M.J.  TILE CONSTRUCTION of a BAC Library and generation of BAC end Sequence-tagged connectors for genome sequencing of the African Autha mosquito Anophales gamble MEDIA Caene. Genomics 268 (6), 720-728 (2003) PUBMED 1265339 COMMENT CASS: AC-ND-137N19, TP.1 COMMENT COLEC-GSS: AC-ND-137N19, TP.1	Department of Enkaryotic Genoalcs The Institute for Genoalcs The Institute for Genoalcs The Institute for Genoalcs The Sol State State Sol State Sol State This 301 838 0208 This Sol State Sol State Sol State This Sol State Sol State Sol State This Solo State State Sol State Solo Solo State Solo Solo State Solo Solo Solo Solo Solo Solo Solo Sol	BASE COUNT	Qy         1298         GACCAGAAGTGCCTCAGGAAGACCTATCTGGCAAGACCTTAACCAGT 1357           HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

FERTURES  L. 732 source  J. 732 J. 733 Source  J. 733 J. 733 Source  J. 743 J.	Owery Match 11.5%; Score 256.4; DB 13; Length 762; Bust Local Similarity 66.4%; Pred No. 6.48-64; Day Matches 368; Conservative 0; Mismatches 166; Indels 0; Gaps 0;	dy 79 citaagaaagtgaaggcagcaccaaaaagagggggggggg	0y 139 CTCGGGATCTIACGCCAACATCATCGCTATCGGAACCCCAAACGACGGGATTTGACTAT 198  174 CTCAACATCCCGCCAGCAACACACACACACACGCGAAGAACTTAACTAC 233	0y 199 GCCGAAGAGTTAAGAAGCTAGATCIGGCAGGGGTTAAAAAGGACCTGGCAGCGCTAATG 258 1	0y   259   ACGANTACAGGGACCACAGATTACGCCCTTCTTATACGC 318
Best   Local Similarity   64.6%;   Pred, No. 6.6e-65;   Indels   0;   Gaps   0;   Matches   387;   Conservative   0;   Mismatches   212;   Indels   0;   Gaps   0;   Conservative   0;   Mismatches   212;   Indels   0;   Gaps   Gassergeaceaccaccaccaccaccaccaccaccaccaccaccacc	dy         450 Tracecorraneananeananearcananea	Qy 510 AGGAAACGTACGTGGAAACTATGACTTAAAACTTTGGTTTTGCAGAGGGGGGGG	0y 570 AGATGTATGGGAGCCTGAAQAAGATGTATACTGGGAGCGGAAACCGGATGGCTGGGAGA 629  Db 562 CGACACATGGGAGCGGAAGATGCTCCTTATACTGGGGTAAACCGCTGTTTGGGAA 621	Qy         630         CANGCGCTATGAAGGTGACCGAGACCTCGAAAATCCCCTGGGAGCCGTACCAATGGGAC         688           1   1   1   1   1   1   1   1   1   1	PRESULT 6 B0752115 B0752115 B0752115 B0752115 B0752115 B0752115 B0752115 ACCESSION B0752115 COllectrichum trifolii SCHRENCE SCHRENCE SCHRENCE SCHRENCE B0752115 COLLECTRICHUM trifolii SCHRENCE B0752115 SCHRENCE SCHRENCE B0752115 SCHRENCE B0752115 SCHRENCE B0752115 SCHRENCE B0752115 SCHRENCE B0752115 A071602 A0

0y   319 ATGGCGTGGCACCGGCACCTACCGTATCGCTGATGGCGTGGTGGCGTCC 378   380 ATGGCGTGGCACCGGCCCGACCTACCGTATCGCTGATGGCTCGTGGTGGTGGTGATCGTGATGGTGTGATCGTGATCGTGATCGATC	RESULT 8 BU065388 BU065388 ACCESSION F94.7_G22_T3 Nitrogen-starved mycella Gibberella zeae cDNA, mRNA ACCESSION F94.7_G22_T3 Nitrogen-starved mycella Gibberella zeae cDNA, mRNA ACCESSION BU065388 VERSION BU065388 VERSION BU065388 CIBBERELIA zeae GIBBERELIA zeae GIBBERELIA ZEAE GIBBERELIA ZEAE TITLE PARGI: ASCOMYCOTE PELICOMYCOTINS, SOTGATIOMYCETES: HYCOCTECHOMYCETES TEALIF TO TAIL PARGIS SOTGATIOMYCETES: ANTHORS TAIL F. AS ANTHORS ANTHORS ANTHORS TAIL F. AS ANTHORS ANTHORS TAIL F. AS ANTHORS ANTHORS TO CAPTOR SOTGATION CONTENT AND SOTGATION CON	M 488	Pred. No. 7.6e-62; Mismatch Carl; 13. AGGTATACGACTGGCCCACH, CCGTCTCGGCCCCACH GGTACTCGGCCCCACH GGTACTCGGCCCACH GGTACTCAAAACACTGAAAGG
DEFINITION ES76334 DSCT COlleCOLICHM TRIFOLII CDNA CLONE DEFINITION ES763334 DSCT COLLECTICHUM TRIFOLII CDNA CLONE DDSCT7-68, MRNA ACCESSION SEQUENCE.  ACCESSION MOTSIBOL. BQ751801.1 G1:21907206 SURRESCON MOTSIBOL.1 G1:21907206 AUTHORS SURRESCON MOTSIBOL.2 MOTSIBO	Seq primer; (gth Ath CgA CtC Act Ath agg C).  Location/bulifiers  Location/bulifiers  Location/bulifiers  Location/bulifiers  Location/bulifiers  Location/bulifiers  Altrain="rocate" the proper make a control and	PASE COUNT 146 a 247 c 130 metal muth X-gal for selection of recombinants.  BASE COUNT 146 a 247 c 130 metal muth X-gal for selection of one of the combinants.  Ouery Match 11.4% Score 254.8; DB 13; Length 707; Best Local Similarity 66.3%; Pred. No. 1.9e-63; Matches 367; Conservative 0; Mismatches 187; Indels 0; Gaps 0; Y 779 ACCANGATCACGGGCACCACACGCGCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACGCCACACCAC	Qy         199 GCGAAAGACTTAAGAAGCTGAGTTAAAAGGACCTGGCAGCGCTAATG         258           1   1   1   1   1   1   1   1   1   1

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AACCCTCTCAGCTGGGCCAGGTTCTCAACGGTCTTGGGAAGTCTCAACCCAGGAGAACTTCAACCCAGGCCAACGGTCTTGGGAGAGTCTTCAACAGGAATTCTCAGAAGTCTTGGAGAGTCTTGGAGTCTTGGTGGCGGGTGTTGTGTGTG	BASE COUNT ORIGIN Query Mat. Best Loca	LT2" "taxon:602" 1173-s13" 1173-s13" 1173-s13" 1183-s13" 119 t 1183 score 244.6; DB 28; Length 918; 18; Pred. NO. 2.3e-60;
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GCGGCGACGGTTCCGAAATTACGGCGCTTCCACAAACGGTGTCAAGCTCGAGCACTTG CTCGTNAACGGGCGCAGCTTCTGGCGCTTCGGCACCAGAAATGACGCTTGGTAGG		950 ACTAGAAGGCGCTGGACCAAGACCCTATGAAGACCAATAACTTTTTGAAAACCT 1019
1) CTATCHACACCCCCAGGTTCTCACCGCCCCGAGATCACCGCTCTGGTCGGT 431 1900 GGTTGGCGTATGGCGACCAACTACCACGTTCGCACTGTTCGAGTGTTTACAAATAAG 1959 111	oy 10 10 27 10	1020 CTTTGGTPACGATGGAGGTPACAGAGGTGGGGGGGGGGGG
1960 CCGGGTCAGCTATCCAATGACTTCTTTGTAAACCTGCTAGACCTCAACACTAAATGGCGA 2019  492 CCTGGTGTTCTGTCCAACACTTCTTCGTCAACCTCCTCAACACCACACGGGGGGGG	0b 2 Qy 11.	204 AAA
552 CCCGTCGCCAACGGCGCCTTCGGGGGTTTGGCCCAAAGACGCAACAAGAG 608 2080 TGGAGTGGCCCCCGGGGGGTTTCGGGGGTATTGACCGCAACAAGAGCGCAACAAGAG 608 1000 TGGAGTGGCCCCGGGTAGACCTGATTCTCGGACCAATCCGAACCTAAGACCCTCGCA 2139	Oy 12	1200 ACGGRACTATGARANGCCTGATGAGTTTGCGGARTGCTTTGCGGARAGGATGGTACAAACT 1259 
609 IGGACIGGIACCGGIGICGACTTIGGAICACACGCTGAGCTCCGCGGACACCT 668 2140 GAAAGTGIACGACGTGCAGATCTGAAGAAAGTTGTT 2178		GRCACACAGAGATATGGGACCAAAGGTGCGCTACCTGGGACCAGAAGTGCCTCAGGAAGA
009 GAGALATATUCTERANCTIGUCISTRACCAGARACCTGGFT:////	Oy 13 Ob 4 Oy 13	1320 CTCATTGGCAAGCCTATACAGTGTAAGCCAACCTCTTGTAGCCAAACGTAT 1379
APO75904 Salmonella typhimurlum LT2, Lambda DASH II Salmonella typhimurlum LT2, Lambda DASH II Salmonella typhimurlum LT3, Lambda DASH II Salmonella typhimurlum genomic cione B173-ff3, genomic survey sequence.  APO75904 APO75904 SSS5904.1 GI:3320774 SSS5904.1 GI:3320774		497 CAA
×	0y 15	1500 ACGTATACGCACTGGCCCCACAAAAAGAACAACACCATCAGCAGTGCCAG 1559
RS Wong, R.MT., Wong, K.K., Benson, N.R. and McClelland, M. Sample sequencing of a Salmonella typhimurium Lr2 lambda library: comparison to the Escherichia coll K12 genomer.  AL FRMS Microbiol, Lett. 173 (2), 411-423 (1999)	9. qq	1560 GGRATICAAAACACHAGAAGGINICCAGGAGGACTITAACCAGGGGGCATCAGNIAACAA 1619 
NE 99243757 ED 10227170 Contact: No Colland M Molecular Biology	Qy 16 Db 7	1620 ACCATANCETGCCCCACCTCATTCTTGCTCCCTCCCCTTCCCGGGGGTCTAGAAAAACTGC 1679 10.
Sidney Kimmel Cancer Center 3099 Science Park Road, San Diego, CA 92121, USA Emal: mcclelland@lifsci.adsu.edu Class: shotgun.	9y 16 Db 7	1680 AAAAGATGCTGGCCATGAGGTGCTGTCAACCGGGACGAGGGAACGCACCGC 1739

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Class: Shorgun.
Class: Shorgun.
1. 918
/organism="Salmoneila typhimurium"
/mol\_type="genomic DNA"

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FEATURES

JOURNAL MEDLINE PUBMED COMMENT

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/clone-*poscr8-27**/
/fissue_type-*mycella*
/day_stage='roung, actively growing mycella (3 days after
fincoularion) grown in liquid culture (cutin minimal medium
clab_hose='basalpas',
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/note="vector: pBluescript SK+; Site_1: EcoRI; Site_2:
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Samech. 10 (Man./M., Town.C.D., Van Aken.S., Utterback,T., Samech. Town.G.D., Collectotichum trifolli race 1

ESYS (From mycella of Collectrichum trifolli race 1

Oppublished Collectrichum trifolli race 1

Oppublished Collectrichum trifolli race 1
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Department of Plant Pathology
University of Minnesora
495 Borlaug Hall, 1991 Upper Buford Circle, St. Par
151 625 635 1243
Pax: 651 649 508
TIGR Sequence name: WTSA127TV More information is
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Location/Qualifiers
1. 742
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BQ751881
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Submitted (16-FB2-2000) Genoscope - Centre National de Sequencage :
Bubmitted (16-FB2-2000) Genoscope - Centre National de Sequencage :
FRANCE (B-FB2-2000) Genoscope - Cons.fr
WW-4genoscope - Cons.fr)
Chasea I to 737)
Direct Submission
Direct Submission
Submitted (16-FB2-2000) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Parla 75015, France
Roux, Parla 75015, France
Collins and sequenced by Genoscope in Collaboration with the
Laboratory of Biochem. and Riol. Molec of Inscots, Institut
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Neopiera; Endopierygota; Diptera; Nematocera; Culicoidea;
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Pred. No. 6e-60;
7; Mismatches 257; Indels 14;
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Anopheles gambiae

    .737
    /organism-"Anopheles gambiae"

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a 217 c 224 g 127
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/strain="PEST"
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Best Local Similarity 62.2%;
Matches 457; Conservative 7
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mgap008x018f.b Magnaporthe grisea Ap Uni-Zap XR Library Magnaporthe grisea cDNs clone mgap008xD18 5', mRNR sequence.
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          Expressed sequence tags of Leptosphaeria maculans, cause of blackled disease of Oilseed Brassloas
of Upublished
Contact: Alexander Indurma Barbara J. Howdett (bhowletteunimelb.edu.au)
School of Botcany
The University of Melbourne, Parkville, VIC, 3010, Australia Tel: 61 3 844 5056
Rex: 61 3 947 5460
Exat: 61 3 947 5460
Exat: 61 3 947 5460
Exat: 73 000 546 Error: 0.00
Seq primer: 73 000 546 Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="v8 mycelial library"
/note="Library prepared from mycelium grown in 10%
Campbell's V8 juice."
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                                                                                                                                                                                                                                                                                /organism="Leptosphaeria maculans"
/mol_type="mkNA"
/strain="M1"
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65.8%; Pred. No. 7.7e-59;
ive 0; Mismatches 180;
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                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:5022"
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1. .562
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Best Local Similarity 65.8:
Matches 347; Conservative
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ECORI; isolate: 28p2; cDNA was prepared from polyymenriche RNA The CNNA was ligated into Lambad gill from Strategene and packaged using Glapack packaging extracts. An aliquot of the amplified library was used to transduce Lecol #1090 and phace DNA was used for transduce lysate. The CNNA inserts were gel purified from a liquid digestion and ligated into pBluescript SK; aliquots of the ligation were used to transform E. Coll DHSalpha which were plated onto medium with X-gal for selection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSJ70112 552 bp mRNA linear EST 09-мAR-2001
LMA123 V9 mycelial library Leptospheeria maculans cDNs clone LMA123
S' similar to putative catalase/peroxidase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                  CTTAAGCAAAGTGCAGGTGGCGGCACCAAAAACAGGGATTGGTGGCCCAACATGCTCAAC 138
                                                                                                                                                                                                                                                                                                                                                                          560 reargarcerescescaaceresceresagreeargestriceasagesesestre 619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 CTCAACATCCTCCGCCAGCACACGCCCGTCACCAACCCGCTGGGCCAGGACTTTGACTAC 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 ATGCCGTGGCACAGCGCCGGCACCTACCGTATCGGTGATGGCCGTGGTGGCGG--TGGCT 376
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Eukaryota, Fangulans
Plosporates, Fungi, nacongcota; Pezizomycotina; Dothideomycetes;
Plosporates; Leptosphaeriacea; Leptosphaeria; maculans complex.
                                                                                                                                                                                                                                                                       DB 13; Length 742;
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                                                                                                                                                                                                                                                                     Score 242.8; DB 13;
Pred. No. 6.9e-60;
0; Mismatches 187;
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Idnurm, A., Cozijnsen, A.J. and Howlett, B.J.
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Best Local Similarity 66.0%;
Matches 367; Conservative
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Best Local &
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DB   366 CAGCGCTGGTACATACCGTGGACGCCGCGGAGGCGGTGGCCAAGGCCAGCAGCGCG 425	RESULT 14 B0751512 LOCUES B0751512 LOCUES LOCUES LOCUES LOCUES LOCUES DEFINITION EXERGING DECT COLletotrichum trifolii cDNA clone pDSCT5-66, mRNA ACCESSION B0751512 B0751512 G01etotrichum trifolii GNGANISM COlletotrichum trifolii GNGANISM COlletotrichum trifolii GNGANISM COLLECTRICHUM TRIFOLII GNGANICON COLLECTRICHUM TRIFOLII GNGANICON COLLECTRICHUM TRIFOLII COND. ON AN ARCH, S., ULLETDACK, T., GNGANICOL COLLECTRICHUM TRIFOLII race I JOURNAL URPUBLISHOR COCHENT COCHENT COCHENT COLLECTRICHUM TRIFOLII TACE I JOURNAL URPUBLISHOR URPUBLISHOR COLLECTRICHUM TRIFOLII TACE I JOURNAL URPUBLISHOR URPUBLISHOR COLLECTRICHUM TRIFOLII TACE I JOURNAL URPUBLISHOR URPUBLISHOR UNIVERTING MINIOSOLI HAN SSION USA MAIN COLLECTRICHUM TRIFOLII TACE I JOURNAL URPUBLISHOR UNIVERTING MINIOSOLIUM MAIN SSION USA MAIN COLLECTRICHUM TRIFOLII TACE I LOCUERUM TRIFOLII 1991 UPPER BUFORG CIRCLE, SE. PAUL, MN SSION, USA	The: 612 625 1343  Pat: 614 625 1343  Pat: 615 69 508  Banil: debbys@puccini.cl.umn.edu
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea) SOURCE Magnaporthe grisea ORGANISM Magnaporthe grisea ORGANISM Particularia grisea SOURCE Magnaporthe grisea Sourdariomycetes; Fungi: Accomycotia: Sordariomycetes; Sordariomycetes; Incertae sedis: Magnaporthaceae; Magnaporthe. Sourdariomycetes incertae sedis: Magnaporthaceae; Magnaporthe. AUTHORS Ebbole D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu,G., Bhatterai AUTHORS Expressed sequence tags from the rice blast fungus, Magnaporthe Grisea JOURNAL Unpublished ON MAR 7, 2002 this sequence version replaced gi:1921758. CONMENT COLLACT: Ebbole DJ Department of plant Pathology & Microbiology Texas AAN University Pathology & Microbiology Peterson Bidg, MS2112, College Station, TX 77843-2132, USA TRIS SOURCE STATE STAT	Chromatogram file of this sequence is available, see contact person fiscar in 4 claboled taken and ille of this sequence is available, see contact person is set in hit (April 127, 2003) gb AAL66352.2  catalase-peroxidase   Neurospora crassa  >4 128921 288 4e-77   Permer	We clieve methods where a null-length alignment to the was trimed according to the alignment, chieving angular was trimed according to the alignment, chieving sequence quality was assessed using phredehrap version 991019 and trimed according to pad files (0.05) and for vector of trimed according to pad files (0.05) and for vector of trimed according to pad files (0.05) and for vector of the set Local Similarity 651% pred No. 2.2e-58;  Matchas 339; Conservative 0; Mismatches 177; Indels 0; Gaps 0; Mismatches 177; Indels 0; Gaps 0; Organizative Conservative 0; Mismatches 177; Indels 0; Gaps 0; Indels 11

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Anotes-Vector: pBluescript SK+: Site.]: EcoRi; Site.2:

EcoRi; isolate: 2ap2: cDNA was prepared from poly*+

EcoRi; isolate: 2ap2: cDNA was prepared from poly*+

EcoRi; isolate: 2ap2: cDNA was lasted or stracts.

An aliquot of the amplified library was used to transduce it out in the amplified library was used to transduce it out it is only into an analysis was purified after EcoRi ligation and ligated into pBluescript SK+. Aliquots of the ligation and ligated into pBluescript SK+. Aliquots of the ligation and ligated into pBluescript SK+. Aliquots of the ligation were plated onto medium with X*qal for selection of
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//close='ppge=mycella'
//dev.stoge='mycella'
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//dev.stoge='mycella'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 AACGATTCTTTGTGAATCTGCTGGACATGGGCACCGAGTGGAAGGCCACGGGCGACGCG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 GAC --- GIGIACGAGGGCAAGGACCGCAGGTCGGCCGAGAAGAAGTGGACGCCGAGCCGG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1618 AAAGCAGTATCGTTGGCCGACCTGATTGTGCTGGCCGGCTGTGCGGGTGTAGAAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 CAGCIGCICACCOTCICGCGCGCGGAACICACGGICCIGCIGGGIGGGIIGCGCGIGCIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2035 GACAAAGTTTTGAAGGCAGAGACTTCAAAACTGGCGAAGTAAAGTGGAGTGGCACCCGG
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 231.2; DB 13; Length 63.1%; Pred. No. 1.7e-56; ive 0; Mismatches 223; Indels
                                    /organism="Colletotrichum trifolii"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 t
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                                                                                                        /strain="race 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 63.1%;
Matches 391; Conservative
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EST632677 DSCT Colletotrichum trifolii cDNA clone pDSCT10-12, mRNA
                                                                                                                                                                                              CTTAAGCAAAGTGCAGGTGGCGGCACCAAAAACAGGGATTGGTGGCCCAACATGCTCAAC 138
                                                                                                                                                                                                                                   259 ACAGATTCACAGGACTGGTGGCCAGCAGTTACGGTCATTATGGCCCCTTCTTTATACGC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 ATGGCGTGGCACAGCGCCGGCACCTACCGTATCGGTGATGGCCGTGGTGGCGGTGGTCC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 GGCTCACAGCGCTTCGCGGCCTCTCAATAGCTGGCCAGACAATGCCAATCTGGATAAAGCA 438
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                                                                                                                                                                                                                                                                                                                         CTCGGCATCTTACGCCAACATTCATCGCTATCGGACCCAAACGACCCGGATTTTGACTAT 198
                                                                                                                                                                                                                                                                                                                                                                                         204 CTCAACATCCTCCCCCCAGCACACCCCGTCACCAACCCGCTGGGCCAGGACTTTGACTAC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGAAGAGTTTAAGAAGCTAGATCTGGCAGCGGTTAAAAAGGACCTGGCAGCGCTAATG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 CGCTTGCTTCTTTGGCCCCATCAAAAAAAAAGGTCGAAAAATCTCCTGGGCGGATCTA 498
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Collectrichum trifolii
Bukaryota: Pund; Ascomycota: Pestizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporio Phyllachoraceae; Collectrichum.
1 (basea 10 613) Town. Town.C.D., Van Aken.S., Utterback,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paul, MN 55108,
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TIGR sequence name: MTSAJ12TK More information is available
                                                                                                                                   ö
                                                                    Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheung, F. and Fraser, C.M. ESTs from mycelia of Colletotrichum trifolii race 1
                                                                                                                               Indels
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Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St.
Tel. 612 625 1443
Pax: 651 649 5058
                                                                    DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                               Pred. No. 4.3e-57;
0; Mismatches 163;
                                                                    Score 233.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualiflers
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BQ752114.1 GI:21907519
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Other_ESTs: EST632678
                                                           Query Match
Best Local Similarity 67.0%;
Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               559 GGTGGCAGAGCAGA 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
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VERSION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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COMMENT
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SOURCE
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ORIGIN
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'n 1677

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509

449

329

269

2214

Search completed: October 8, 2003, 15:29:20 Job time: 4640.63 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

; Search time 60.1769 Seconds (without alignments) 1965.061 Million cell updates/sec 7, 2003, 19:31:22; October

Run on:

US-09-884-889-8

4002 1 MENHKHSGSSTYNTNTGGKC.....VKDFVKANAKVMDLDRFDLK 745 Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A. Carlos 1, 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 1975 | 197 A\_Geneseq\_19Jun03:\* 1; /STR01'-

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gcgdata/geneseg/genesegp-emb1/AA2003.DAT:\*

## SUMMARIES

	Description	Microscilla furves	Mycobacterium tube	Mycobacterium tube	M. tuberculosis ca	M. tuberculosis ca	Alcaligenes (Deley	Alcaligenes catala	M.tuberculosis H37	M.tuberculosis kat
	ΠD	AAW33810	AAW26596	AAW31343	AAW95398	AAW95399	AAW33809	ABG33040	AAR43670	AAW78363
	8	19	18	13	20	20	19	53	14	50
Query	Length	745	740	740	740	740	753	753	735	735
Query	Match	100.0	63.6	63.6	63.6	63.5	57.2	57.2	56.9	56.9
	Score	4002	2544	2544	2544	2541	2290.5	2290.5	2278.5	2278.5
Result	2	1	~1	æ	•	'n	9	7	80	đ

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#### ALIGNMENTS

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Microscilla furvescens catalase-53CA1.
      AAW33810 standard; Protein; 745 AA.
                    (first entry)
                   18-NOV-1998
             AAW33810;
RESULT 1
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Catalase; epoxidation; hydroxylation; biosensor; paper bleaching; pasteurisation

Microscilla furvescens,

WO9800526-A1 08-JAN-1998

97WO-US16513 96US-0674887 03-JUL-1997; 03-JUL-1996;

Sanyal I; (RECO-) RECOMBINANT BIOCATALYSIS INC. Adhikary RS, Robertson DE,

WPI; 1998-086953/08. N-PSDB; AAV06555 New bacterial catalases, related nucleic acid vectors and transformed cells - used as oxidising agents and for detecting or

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2 ENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPND 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This polyapetidas comprises a consequence of the Wychbacterium Luberculosis wild-type canalase-perxidase engame of the Wychbacterium cuberculosis of rapidly describing strains of M tuberculosis which are nesterant to the tuberculosis contained from the discovery of A mutualiosis in the wild type kat gene sequence the discovery of A mutualiosis in the wild type kat gene sequence contained to the central from the addition of debellon of restriction endomulesse sites. Frimers (see AMT90410) are provided for the present in the principle of the present contained from a test M: tuberculosis strain and further principle gene from a test M: tuberculosis strain have determination of the susceptibility to the strain. (Updated on 25-AMX-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining susceptibility of Mycobacterium tuberculosis strains to isoniazid - by detecting mutation(s) in the catalase-peroxide gene,
                                                                                                                                                                                                                                                            iconiazid resistance, restriction fragment length polymorphism;
RTFP, kng gene, catalase, peroxidase, multiple drug resistence;
isonicotinic acid hydrazide; IRR; tuberculosia; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               confers INH resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             confers INH resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "mutation to Leu confers INH resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "mutation to Thr confers INH resistance"
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                                                                                                                                                                                                                 Mycobacterium tuberculosis wild-type catalase-peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Column 31-36; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualiflers
                                                 AAW26596 standard; Protein; 740 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- "mutation 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ďR;
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94US-0228662.
                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                (updated)
(first entry)
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Matches 480; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cockerill FR, Kline BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAYO-) MAYO FOUNDATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-424226/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       740 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                        tuberculostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                             25-MAR-2003
21-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1997
                                                                                                  AAW26596;
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Best Local 8
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      RESULT 2
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421 THRDMGRYNYLGEPVPQEDLINODPIEDVSHPLYDENDIEGLKAKILESGLIVSELVST 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                  The present sequence is of the Microscilla furvescens catalase-53CAL. Catalase-53CAL may be used to catalase oxidation reactions such as covatiation or hydroxylation. The enzyme can also be used to detect of security hydrogen pecudie. e.g. in connection with silvoxilla acid security by the contact and the silvoxillation of security contact and change publisher bleaching and pecucial and the silvoxillation of the contact and change of the contact and contact 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DPDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGGGGSGSGRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KPDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 SLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIRPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQBGVFTNKPGQLSND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNG
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                                                                                                                                                                                                                                                                                                                                                                               DB 19; Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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   e.g. in biosensors
                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 4002;
100.0%; Pred. No. 0;
ive 0; Mismatches
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destroying hydrogen peroxide,
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100. Matches 745; Conservative
                                                                                                                                                                                                                                                                                                                              745 AA;
                                                                                                                                                                                                                                                                                                                                    Sequence
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This protein sequence represents the concensus amino acid sequence of the ketc gene factor and Wochbartchiam tuberculosis stinis 813PW MC, ARCC 25518, ARCC 3724, GAIO8 ARI35912, LG67.92, ARI68372, ARIJ180, ARIA1900, ARIJ1804, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 AAFDYAAEVATIDVDALTRDIEEVMTTSQPWWPADYGHYGPLFIRMAMHAAGTYRIHDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540 KAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 TFGFGFGRVDQWEDDE-VYWGKEATWIGDERYSGRRDLENDLAAVQMGLIYVNPEGPNGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAGTIPDAH-DPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THRDMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600 NYIKPEHKYSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 TFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                      Determination of isoniazid sensitivity of Mycobacterium tuberculosis strains - by restriction length polymorphism analysis of katG gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.6%; Score 2544; DB 19;
Best Local Similarity 64.3%; Pred. No. 1.4e-215;
Marches 480; Conservative 88; Mismatches 168;
                                                                                                                                                                                                       Example 2; Column 15-20; 18pp; English.
                                                Ę,
                                            잼
                                            Kline BC,
(MAYO-) MAYO FOUNDATION.
                                                                                         WPI; 1998-007975/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 740 AA;
                                            Cockerill FR,
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                                                                                                                                                                                                TFGFAGGRADVWEPEEDVYWGAETEWIGDKRYEGDRELENPIGAVQMGLIYVNPEGPNGK 241
                                                                                                                                                                                                                                                                                          PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMS 301
                                                                                                                                                                                                                                                                                                                 LGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKD 361
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                                                                                                                                                                                                                             242 PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catalase-peroxide; katG; mutation; isonicotinic acid hydrazide; INH; tuberculosis; diagnosis; detection; variant.
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DAQPKEVQDEVAAWDKVMNLDREDVR 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention realtes to a novel method of detecting Mycobacterium buberculosis. The method comprises amplifying the DMA in the samples to generate a detectable amount of amplified DMA comprising a catalase.

Derivate (Rato) DMA fragment with sequence of bases 904-1523 of the PMA tuberculosis strain H37Rw MC katG gene sequence. The method optionally current comprises determining if the AtC DMA fragment has a serine to threonine mutation in code of 15 (8313T mutation). Indicative of an color of intended (IMH) resistant W. tuberculosis strain. The method can be used dydrated (IMH) resistant W. tuberculosis ration. The method can be used to detect W. tuberculosis in biological fuluis, composed the man sputum useful to disquose tuberculosis. This disease is a major cause of human morbidity and mortality, and conclusive disquosis and subsequent treatment depends on identification of the attologic agent W. tuberculosis. The intended allows such drug resistant strains have amerged; the method allows such drug resistant strains to be identified. The present sequence represents the wild-type M. tuberculosis kate of product.
PDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGR 121
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                                                                                                                                                                                                                                                                                                                                                                                     Catalase-peroxide; katG; mutant; mutation; isonicotinic acid hydrazide; INH; tuberculosis; diagnosis; detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of Mycobacterium tuberculosis - by amplifying katG gene
and detecting specific fragment, and optionally identifying
INH-resistant strains by detecting specific mutation
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    M. tuberculosis catalase peroxide (katG) gene product.

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Matches 480; Conservative 88; Mismatches 168;
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                                                                                                   715 DAQPKFVQDFVAAWDKVMNLDRFDVR 740
                                                                                   DSEEKFVKDFVKAWAKVMDLDRFDLK 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                        (first entry)
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The remains is the method comprises amplified DNA in the sample to generate a detectable amount of samplified DNA to comprise a smoult characterized a detectable amount of samplified DNA to comprise a smoult of the sequence of bases 904-132 of the remainment of samplified DNA comprises a train size with sequence of bases 904-132 of the remainment of sample of the second of the 
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                                                                                                                                                                                                                                                                                                                                                             Detection of Mycobacterium tuberculosis - by amplifying katG gene
and detecting specific fragment, and optionally identifying
INH-resistant strains by detecting specific mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page -; 83pp; English.
                              97US-0852219
                                                                                                                                                                              Cockerill FR, Kline BC,
                                                                                                      MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                 MPI; 1999-070099/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           740 AA;
                                                                                                                                                                                                                                                                                          N-PSDB; AAX00818
                              07-MAY-1997;
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GAGAGTIPDAH-DPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKL 420 421 THROMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVST 480 PDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPPFIRMAWHSAGTYRIGDGR 121 GGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFK 181 TFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGK 241 PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMS 301 LGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKD 361 EQHPPITETITGAASNG-CPVVGHMKYPVEGGG--NQDWWPNRLNLKVLHQNPAVADPMG 59 2 ENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPND 61 Gaps 10; 63.5%; Score 2541; DB 20; Length 740; 64.2%; Pred. No. 2.6e-215; ive 89; Mismatches 168; Indels 10 Local Similarity 64.2 867 362 Query Match 242 302 Matches 셤 g à Š 셤 ç 셤 à g à 셤 ò ð

595 629 655 599 DFFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCA 719 AWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQ-QLARVLKTLEGIQEDFNQAQSDN 539 AWAAASSFRGSDKRGGANGGRIRLQPQVGWEVNDPDGDLRKVIRTLEEIQESFNSAAPGN 535 NY I KPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSN KAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFR 720 DSEEKFVKDFVKAWAKVMDLDRFDLK 745 481 g à g ò g à g à 용

Ź AAW33809 standard; Protein; 753 AAW33809; AAW33809

Alcaligenes (Deleya) aquamarinus catalase-64CA2.

18-NOV-1998 (first entry)

Catalase; epoxidation; hydroxylation; biosensor; paper bleaching; pasteurisation.

Alcaligenes aquamarinus. WO9800526-A1. 38-JAN-1998.

96US-0674887. 97WO-US16513. 33-JUL-1997; 03-JUL-1996; 

(RECO-) RECOMBINANT BIOCATALYSIS INC

Sanyal I; Adhikary RS, Robertson DE,

WPI; 1998-086953/08. N-PSDB; AAV06554 New bacterial catalases, related nucleic acid vectors and transformed cells - used as oxidising agents and for detecting destroying hydrogen peroxide, e.g. in blosensors

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Claim 1; Fig 1; 35pp; English.

The present sequence is of the Alcaligenes aquamarinus catalase-64CA2. Outsiaes-64CA2 may be used to catalyse ordistion reactions such as epoxidation or hydroxylation. The enzyme can also be used to detect destroy hydrogen perzitle. 9, in connection with 91/xxylla scid perduction. Dioesnors, contact a season to perpending the perduction of dairy products. An intendist stated against partial and purification of calls containing the purification of calls containing the purification of calls containing the encoding catalase-64CA2 can be used to accept the production and purification of calls containing the enzyme. Fragments of the gene encoding catalase-64CA2 can be used to identify related sequences.

753 AA; Sequence

Gaps Length 753; 25; Indels Query Match 57.2%; Score 2290.5; DB 19; Bet Local Similarity 59.1%; Pref. No. 3.8e-133; Matches 433; Conservative 92; Mismatches 183; II

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                                                                                   PDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETWGFKTFGFAGGRADVWEPEE 197
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                                                                                                                                                                                                                                                                                                        LGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVSTAWASASTFRNS 491
                                                                                                                                                                                                                                                                                                                                                DKRGGANGARIRLAPOKDWEVNNPQOLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVLA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNIJDLNTK 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVKDFVK 731
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GKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKKLDLAA
                                                                                                                                                                                     274 LETFARMAMNDEKTAALTAGGHTVGNCHGNGNASA-LAPDPKASDVENQGLGWGNPMQG
                     GKCPVMHGG----NTSTGTSNKDWWPEGLNLDILHQQDRKSDPMDPDFNYREEVRKLDFDA
                                          VKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGGGGGGRFAPLNSW
                                                                                                DVYWGAETEWL--GDKRYEGD----RELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDI
                                                                                                                                                    DIYMGDEKEWLAPSDERY-GDVNKPETMENPLAAVOMGLIYVNPEGVNGHPDPLRTAQQV
                                                                                                                                                                         RETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWRNTYGTG
                                                                                                                                                                                                                                                                                                                    HDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRY
                                                                                                                                                                                                                                                                                                                                                                                           GCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalase; hydrogen peroxide; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AWAKVMDLDRFDL 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss; marine bacteria;
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This invention relates to the DNA and protein sequences of a novel control and acadase polypertide. The protein of the invention or its homologue is useful for catalysing the broakdown of hydrogen peroxide. The protein sequence of the invention is useful for modifying amail conclosules, by mixing the protein or its fragments with a small molecule. The protein of the invention is also useful for catalysing blochemical reactions, for hydrolysing a slow side of the invention is a solice useful for catalysing blochemical reactions, for hydrolysing specifically to the protein. The nuclects acid sequences of the specifically to the protein. The nuclect acid sequences of the sections is useful as a probe to determine whether a blockpical sample, such as a soll sample, contains an organism having the nuclect acid or such as a soll sample, contains an organism having the nuclect acid or such as a soll sample, contains an organism having the nuclect acid or such as a bold such as useful in immunooff finity charactography. Procedures to isolate or purify the protein or for detection of protein or for detection of protein or function is useful in immunooff finity, and expected in the invention is beat table; is heat resistant, and is able to contain sample, and is and the contains and protein of the invention is heat table; is heat resistant, and is able to contain sample, and is also to contain sequence and regal activity after exposure to temperatures of from advantance protein of the invention of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGSGSQRFAPLNSW 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDNANLDKARLLLWPIKOKYGRKISWADLMILTGNVALETMGFKTFGFAGGRADVWEPEE 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 SDPSIRHNPIMTDADMAIKVNPTYRAICEKFMADPEYFKKTFAKAWFKLTHRDLGPKSRY 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEBFKKLDLAA 77
                                                                                                                                                                                                                                                             New purified catalase polypeptide useful for catalyzing the breakdown of hydrogen peroxide, for modifying small molecules, and for generating antibodies which bind to the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVYWGAETEWL--GDKRYEGD----RELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.2%; Score 2290.5; DB 23; Length 753; 59.1%; Pred. No. 3.8e-193;
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                                                                                                                                                                   Adhikari R;
                                                                                                                                                                                                                                                                                                                                                  Claim 22; Fig 5; 44pp; English
96US-0674887.
97US-0951844.
99US-0412347.
                                                                                                                                                                Sanyal I,
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hes 433; Conservative
                                                                                 ROBE/) ROBERTSON D E.
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                                                                                                  (SANY/) SANYAL I.
(ADHI/) ADHIKARI R.
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                                                                                                                                                                Robertson DE,
03-JUL-1996;
16-OCT-1997;
05-OCT-1999;
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Gaps

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236 300 295 360 355 419 413 479 472 539

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DFFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCA 719
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                                                                                                                                                                                                                                                                                                                              GGGGSGSQRFAPINSWPDNANLDKARLLLWPIKOKYGRKISWADLMILTGN-VALETMGF
                                                                                                                                                                                                                                                                                                                                             180 RRSGSASG-VDQWETDE-VYWGKEATWLGDDGYSVS-DLENPLAAVONGLIYVNPEAPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                        241 KPDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 DGAGAGTIPDPFGGPGRS--PTMLATDLSLRVDPIYERITRRWLEHPEELADEFRKAWYK
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                                                                                                                                                                                                                   2 ENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPND
                                                                                                                                                                                                                                    EQHPPITETTTGAASNG-CPVVGHMKYPVEGGG--NQDWWPNRLNLKVLHONPAVADPMG
                                                                                                                                                                                                                                                                                        181 KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNG
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the me with high coding probability: a 715 anno acid protein is encoded by the ORP having predicted mol. wt. 80029. This protein conforms to the structure of Known bacterial catalises peroxidaes which consist of two modules (possibly the result of a depictation event), both slowing founding (possibly the result of a depictation recent), both slowing founding to the yeast enzyme, fused to a unique the kntl as agence of about 50 annian acid residues, whentions in the kntl agenc on result in loss of IMM-susceptibility, it. the the formation of antibiotic resistent Wpobacterial strains
                                                                                                                                                                 DB 14; Length 735;
                                                                                                                                                                                           Indels
                                                                                                                                                                                         81; Mismatches 201;
                                                                                                                                                               56.9%; Score 2278.5; DB 14 60.2%; Pred. No. 4.2e-192;
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                                                                                                                                      735 AA;
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                                                                                                                                                                        IGPEVPAEDLIMODFIFAGNIDYCE----EVVKQKIAQSGLSISEMVSTAWDSARTYRGS
                                                                                  WRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVKDFVK
              LGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVSTAWASASTFRNS
                                                                   DKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVLA
                                                                                                                     GCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The katG gene of Mycobacterium tuberculosis was isolated on a KpnI fragment by shotgun cloning. The sequence contains one open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catalase-peroxidase; isonicotinic acid hydrazide; isoniazid; INH; antibiotic; susceptibility; sensitive; resistant; katG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoniazid, rifampicin or streptomycin resistance in tuborculosis
y detecting mutation in katG, rpoB or rpsL genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rapid detection of antibiotic resistance in Mycobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telenti A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis (strain H37Rv)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.tuberculosis H37Rv catalase-peroxidase.
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                                                                                                                                                                                                                                                                                                                                                                              AAR43670 standard; Protein; 735 AA
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UNIV CURIE PARIS VI P & M.
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(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDI-) MEDICAL RES COUNCIL
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                                                                                                                                                                                                                                                                                   AWAKVMDLDRFDL 744
                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
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Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ51531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09322454-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
17-MAY-1994
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14-AUG-1992
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DGAGAGTIPDAH-DPSKSHAPFMLTTDLALRNDPDYEKISRRYYENPDEFADAFAKAWYK 419
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                                                                                 DGAGAGTIPDPFGGPGRS -- PTMLATDLSI, RVDPIYERITRRWLEHPEELADBFRKAWYK 413
                                                                                                                              LTHRDMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVS 479
                                                                                                                                                               414 LIHRDMGPVARYLGPLVPKQTLLWQDPVPAVS-TTSSAKQIASLKSQIRASGLTVSQLVS 472
                                                                                                                                                                                                         TAWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDN 539
                                                                                                                                                                                                                                              TAWAAASSFRGSDKRGGANGGRIRLOPOVGWEVNDPDGSAQCHSHPEEIQESF -- TRRGN 530
                                                                                                                                                                                                                                                                                        540 KAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFR 599
                                                                                                                                                                                                                                                                                                                            531 IKVSFADLVVLGGCAPLEKAAKAAGHNITVPFTPGPHDASQEQTDVESFAVLEPKADGFR 590
                                                                                                                                                                                                                                                                                                                                                                      NYIKPEHKVSAEEMLYDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSN 659
                                                                                                                                                                                                                                                                                                                                                                                                             NYLGKGNRCRPSTSLLDKANLLTLSAPEMTVLVGGLRVLGANYKRLPLGVFTEASESLTN 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 GLGWKSSYGTGTGKDAITSGIEVVWTNTPTKWDNSFLEILYGYEWELTKSPAGAWQYTAK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining the ability of a compound to remove a reactive oxygen species (ROS), useful in pharmaceutical and nutraceutical fifelds and measuring activities of antioxidants, comprises providing a cell having measuring activities of antioxidants, comprises providing a cell having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catalase; KatA; reactive oxygen species; ROS; ROS-inducible promoter;
H2O2 level; antioxidant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of Agrobacterium tumefaciens catalase KatA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720 DSEEKFVKDFVKAWAKVMDLDRFDLK 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 TRQAKEVTGEVAAMDKVMNLDRFDVR 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 63-67; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB78212 standard; Protein; 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001US-266657P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a ROS-inducible promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEM 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ENHKHSGSSTYNTINTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQHPPITETTTGAASNG-CPVVGHMKYPVEGGG--NODWWPNRLNLKVLHQNPAVADPMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGN-VALETMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRSGSASG-VDQWETDE-VYWGREATWLGDDGYSVS-DLENPLAAVQMGLIYVNPEAPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the catalase peroxidase enzyme encoded by the Mysobotcarium tuberculosis katelogene. The gene was asolated from a M. tuberculosis strain resistant to isonicothnic acid hydrazlde (troinsing or MH). The sequence is useful in the diagnosis of tuberculosis caused by IMH: resistant M. tuberculosis and in the (Updated on 70-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding catalase-peroxidase HPI - useful for rapid identification of isoniazid resistant Mycobacterium tuberculosis
                                                                                                                                            catalase; peroxidase; enzyme; isonicotinic acid hydrazide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.9%; Score 2278.5; DB 20; Length 735; 60.2%; Pred. No. 4.2e-192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang Y;
                                                                                                                                                               diagnosis; resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 10A; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                95US-0459499.
92US-0875940.
92US-0929206.
93US-0029655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole ST, Heym B, Young DB,
                                                                                               M.tuberculosis katG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                                                                                         95US-0459499
                                       (updated)
(first entry)
                                                                                                                                                                                                      Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX16963
                                                                                                                                                               isoniazid; INH;
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30-APR-1992;
                                       20-MAR-2003
11-MAY-1999
                                                                                                                                                                                                                                           JS5871912-A
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Matches 449;
AAW78363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                         satG;
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DPDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 ELTKSPAGAYQWKPKDGAGAGTIPDAHDPSKSHAPFMLTTDLALRMDPDYEKISRRYYEN 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KILESGLTVSELVSTAWASASTFRNSDKRGGA-NGARIRLAPQKDWEVNNPQQLARVLKT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MENQ------NRQNAAQCPFHESVINGSS-NRIINKDWWPNQLNLSILHQHDRKINPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 ICSFWRAMSLINRWVEKRIDSAAGPLTSGIRKKTFIGDRKKSGSPLNAIPV-IATSKTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDEFADAFAKAWYKI,THRDMGPKVRYI,GPEVPQEDLIWQDPIPDVSHPLYDENDIEGLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 RGGASTGTQRFAPLNSSPDNANLDKAR-----RCYGRS-----KRNTGTKSLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 FKTFGFAGGRADVW-EPEEDVYWGAETEWLGDKRYEGDRELE-NPLGAVQMGLIYVNPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 PRANGVNLROPRRAGROAGSKSRGISAETFRRMGMKDEETVALIAGGHTFGKAHRGGPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 KYVGREPAAAGIEEMSLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 731;

    genetic information of heat resistant peroxidase -
culturing transformant and collecting heat resistant

                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat resistant peroxidase may be produced from a plasmid por
transformed E.coll UM228 expression system efficiently and
in Large quantities.
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89; Mismatches 227; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.5%; Score 1699.5;
                                                   Heat resistant peroxidase gene product.
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 8pp; Japanese
                                                                                                                                                                                                                                        89JP-0089469
                                                                                                               Bacillus stearothermophilus
                                                                                                                                                                                                          89JP-0089469
                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 48.38
Matches 374; Conservative
                                                                                                                                                                                                                                                                                                    WPI; 1990-372008/50
                                                                               poD10; E.coli UM228
                                                                                                                                                                                                                                                                      (TOYM ) TOYOBO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          731 AA;
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ06815
                                                                                                                                           JP02268684 -A.
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                   06-MAR-1991
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a ROS-inductole promoter operably linked to a resporter gene that is heterologous to the promoter, and exposing the cell to a compound potentially abla to remove the ROS. The method is useful in determining the ability of a compound or gene product to remove a ROS and determining the level of the ROS HIZO laide a cell, to properly assess and abeliant the level of the ROS HIZO laide a cell, to properly assess and abeliance articolated may also be used in selecting for new or improved ROS citys. The method may also be used in selecting for new or improved ROS.
                                                                                                                                                                                                                                                                                                                                                                                               185
                                                                                                                                                                                                                                                                                                78 VKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGGGGGGRAPLNSW 137
                                                                                                                                                                                                                                                                                                                                                              PDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFKTFGFAGGRADVWEPEE 197
                                                                                                                                                                                                                                                                                                                                                                                                                             251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : ::||||||| ::||||||| 652 WVPT--GNNLYEIRDRRTGAARYSATRVDLVIGSNSILRAYAEVYAQDDNREKFARDFIA 709
                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                  9 GKCPVMHGG----NTASGKSVTEWPNALNLDILHQHDTKTNPLGTSFNYREALKTLDVEA 65
                                                                                                                                                                                                                                                                                                                          LKADLRALMTDSQEWWPADWGSYVGMMARYTWHAAGSYRVTDGRGGANTGNQRFAPLNSW
                                                                                                                                                                                                                                                                                                                                                                                18 GKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKKLDLAA
                                                                                                                                                                                                                                                                                                                                                                                                                           DVYWGAETEWL - - GDKRYEGD - - - - RELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDI
                                                                                                                                                                                                                                                                                                                                                                                                                                              RETFCKMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 IGRDTVVSGIEGAWISEPIKWDNGFFDMLFKHEWILTHSPAGASOWAPITIAEEDKPVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 GCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTK
                                                                                                                                                                                                        Gaps
                                                                                                                                                                       Length 723;
                                                                                                                                                                                                        25;
                                                                                                                                                                                                      88; Mismatches 197; Indels
                                                                                                                                                                          DB 23;
                                                                                                                                                                                         Pred. No. 2.7e-185;
                                                                                                                                                                       55.0%; Score 2201.5;
57.7%; Pred. No. 2.7e
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                                                                                                                                                                                                      Matches 423; Conservative
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|| |||| ||||
710 AWTKVMNADRFDL
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                                                                                                                                         723 AA;
                                                                                                           scavengers
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                                                                                                                                         Sequence
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                                                                                                                                                                          Query Match
                                                                                                                                                                                         Local
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328 TPTOWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGGTIPDAHDPSKSHAPFMLTTDL 387
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                                                                                                                                                                                                                                                                                                                                                                                                  PD-VSHPLVDENDIEGLKAKILESGLTVSELVSTAWASASTFRNSDKRGGANGARIRLAP 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTRTGDVTRRQPI-RALPVLEKIQKESGKA-----SLADIIVLPGLFVVEKSASAAGL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    626 PEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTKWRASDESDKVFEGR 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           686 DFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVKDFVKAWAKVMDLDRFDL 744
diagnostic amino acid sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.Wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                          244 PQPIYNP -- TEQDIIDLKFAIADSGLSVSELVSVAWASASTFRGGDKRGGANGARLALMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q-KDWEVNNPQQLARVLKTLEGIQEDPNQAQSDNKAVSLADLIVLAGCAGVEKAAKDAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 EVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAEEMLVDRAQLLSLSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                              14;
                                                                                                                                                     Length 533;
                                                                                                                                                                                              Indels
                                                                                                                                                   31.6%; Score 1266; DB 22;
                                                                                                                                                                                              95;
                                                                                                                                                                       55; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #8814.
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2000US-0649167
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                                                                                                                                                                                           Conservative
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N-PSDB; AAS73010.
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                                                                                                                                                                       Similarity
                                                                                                          533 AA;
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23-AUG-2000;
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                                                                                                          Sequence
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                                                                                                    629
                                                                                                                                             608
                                                            LRGHPARTAEKSKHRRLDRLGGTLRWKRQPATPALMSNCHFSLAAAMRHKSKPMSKALPC 570
                                                                                                                                                                                                            WNRSQMASAT-----SADRPRND
                                                                                                                                                                                     ALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTKWRASDESDKVFEGRDFKT
                       LEG----IQEDFNQAQSDNKAVSL-----ADLIVLAGC----AGVEKAAKDAGHEVQV
                                                                                                    PFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAEEMLVDRAQLLSLSAPEMT
                                                                                                                                                                                                                                                                         GEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVKDFVKAWAKVMDLDRFDL 744
                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypoptides, useful in adaptostics, forensics, one mapping, identification of mutations responsible for genelic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 55416; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #25048
                                                                                                                                                                                                                                                                                                                                                                                                                ABG25057 standard; Protein; 533 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
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23-AUG-2000;
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To propepted (II) sequences (II is useful as hybridisation probes, polymericae chair sequences (II is useful as hybridisation probes, polymerase chair sequences (II is useful as hybridisation probes, polymerase chair sequences are sequences as expressed sequence tags of or identifying spreased sequences as expressed sequence tags of interaction formal and activity of (II) is useful in sease as tags involving (III). (II) as useful or interaction or identifying as the seprement of interaction or identifying or interaction or interaction or interaction or interaction or identifying abertal protein expression or bloodycal activity of interactions in interactions in interactions or interactions in the pulypeptic and polymerate protein expression or bloodycal activity or interactions and to produce other types or other traits to assess bloodycestity and to produce other types or other traits to assess bloodycestity and to produce other types or other traits to assess bloodycestity and to approach and produce other types or other traits to assess bloodycestity and and produce other types or other traits to assess bloodycestity and and activity and sequences of the and products dependent on but and dispusative and no acts sequences of the inventions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WiPo af ttp. W.Po. Inc./pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 ALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRYLGPEVPQEDLIWQDPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 TPTOWSNYFFENLFRYEWVOTRSPAGAIQFEAVD - APELIPDPFDPSKKRKPTMLVTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 TPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGAGTIPDAHDPSKSHAPFMLTTDL
                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in adapostics, foremsics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.9%; Score 675; DB 22;
60.9%; Pred. No. 1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 39656; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #8819.
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                                                                                                                                                                                                                                    Tang YT;
    30-MAR-2001; 2001WO-US08631.
                                                                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 137; Conservative
                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                     WPI: 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1550 AA:
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                                                                                                                                                                       HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS73484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blodiversity
                                                                                                                                                                                                                                    Drmanac RT,
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                                                                                                                                                                                          to pupperfied (II) sequences (II) is seful as hybridistin probas, polymerase chain reaction (PCR) primers, oligomers and for chromosome and gene amplitury, and in recombinant production of (II) the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 KAKILESGLIVSELVSTAWASASIFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLK 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVEAFEALEPAADGFRNYIKPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYD 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSQHGVFTNKPGQLSNDFFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIF 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO att ttp.w.lpo.lmc/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             524 TLEGIQEDFNQAQSDNKAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
responsible for genetic disorders or other traits and to assess blodiversity .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.1%; Score 883.5; DB 22; Length 273; 62.6%; Pred. No. 2.2e-69; ive 39; Mismatches 57; Indels 9;
                                                                                                                                                                   invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                704 GSNSELRALAEVYGCADSEEKFVKDFVKAWAKVMDLDRFDL 744
                                                                                                 Claim 20; SEQ ID No 39182; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #9288.
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Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40200175067-A2
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387 585 447 645

Gaps

703

Search completed: October 7, 2003, 19:42:23 Job time : 63.1769 secs

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us-09-884-889-8.rag

54

42; Indels 74; Gaps

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The invention relates to isolated polynuclectide (I) and objepetide (II) sequences. (I) is useful as hybridistation probes, polymerae chain resction (PCR) primers, oligomers, and for chromosome opinuclectides are chain resculping treochabinate production of (II). The polynuclectides are also used in diagnostics as expressed expense to rescore normal activity of (II) or to treat disease states involving to rescore normal activity of (II) or to treat disease states involving to uncitating a polypeptide in tissue, as molecular weight makers and as quantitating a polypeptide in tissue, as molecular weight makers and as tood supplement. (II) and its binding partners are useful for treating the polypeptide and of the interpretation critical activity. The polypeptide and polynuclectide sequences have applications in the polypeptide and polynuclectide sequences have applications in cresponsible for genetic disorders of other traits to assess biodiversity and to produce other types of data and products dependent on DNA and activity and to produce other types of data and products dependent on DNA and activity and to activity and the polyperical activity is and to produce other types of data and products dependent on DNA and the polyperic and and products dependent on DNA and the data page and to activity and sequences. Applicances of the invention over the data and product dependent on DNA and the data and product dependent on DNA and the data and product activity and the data and activity and data and product activity and and activity and data and product activity and and activity and data and activity and and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
Human; chromosome mapping; gene mapping; gene therapy, forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
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GenCore version 5.1.6
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OM protein - protein search, using sw model

(without alignments) 1440.492 Million cell updates/sec October 7, 2003, 19:40:18; Search time 21.8825 Seconds Run on:

Title: Perfect score:

Sequence:

1 MENHKHSGSSTYNTNTGGKC.....VKDFVKAWAKVMDLDRFDLK 745 US-09-884-889-8 4002

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

328717 segs, 42310858 residues Searched:

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2\_5/ptodata/1/laa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/5E\_COMB.pep:\*
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/cgn2\_6/ptodata/1/laa/6E\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/6E\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/fep Issued\_Patents\_AA:\*

Pred. Mo. 1s the number of results predicted by chance to have a acces greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Appli	Appli	Appli	App11	I, Appl	Appli	Appli	Appl	Appl	3, Appl	3. Appl	), Appl			8115, Ap	Appli	Appli	Appli	8, Appl	Appli	3, Appl	2, Appl	3. Appl			-	5, Appl
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	Description	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sednence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMITTES	ID	US-08-674-887A-8	US-08-951-844-8	US-09-412-347-8	US-08-418-782-7	US-08-418-782-21	US-08-228-662-7	US-08-852-219-7	US-08-852-219-21	US-08-313-185-49	US-08-459-499-13	US-09-082-614A-49	US-08-313-185-50	US-08-459-499-14	US-09-082-614A-50	US-09-328-352-8115	US-08-674-887A-6	US-08-951-844-6	US-09-412-347-6	US-08-313-185-48	US-08-459-499-9	US-09-082-614A-48	US-08-459-499-12	US-08-313-185-53	US-08-459-499-17	US-09-082-614A-53	US-08-313-185-51	US-08-459-499-15
	DB	7	٣	4	4	H	-	7	~	~	~	m	7	~	٣	4	7	m	4	N	~	m	~	ď	N	٣	N	C)
	Query Match Length DB	745	745	745	740	740	740	740	740	726	726	726	729	729	729	726	753	753	753	735	735	735	735	652	652	652	731	731
*	Query Match	100.0	100.0	100.0	63.6	63.6	63.6	63.6	9.69	60.5	60.5	60.5	59.9	59.9	59.9	58.2	57.2	57.2	57.2	56.9	56.9	56.9	56.7	48.8	48.8	48.8	44.0	44.0
	Score	4002	4002	4002	2544	2544	2544	2544	2544	2421.5	2421.5	2421.5	2397	2397	2397	2331	2290.5	2290.5	2290.5	2278.5	2278.5	2278.5	2270.5	1954	1954	1954	1760.5	1760.5
	Result No.	П	ď	3	4	S	9	7	80	6	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Sequence 51, Appl	Sequence 52, Appl		Sequence 16, Appl	Sequence 4, Appli	44	4 .	44	Sequence 6, Appli	m	Sequence 6, Appli	Sequence 3, Appl1	Sequence 5, Appli	Sequence 8, Appl1	Sequence 2, Appl1	Sequence 5, Appli	7	7
US-09-082-614A-51	US-08-313-185-52	US-09-082-614A-52	US-08-459-499-16	US-07-929-206-4	US-08-313-185-44	US-08-459-499-4	US-09-082-614A-44	US-07-929-206-6	US-08-313-185-3	US-08-459-499-6	US-09-082-614A-3	US-07-929-206-5	US-07-929-206-B	US-08-313-185-2	US-08-459-499-5	US-09-082-614A-2	US-07-929-206-2
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731	293	293	294	78	7.8	7.8	78	37	37	37	37	37	37	37	37	37	120
44.0	7.8	7.8	7.8	5.5	5.5	5.5	5.5	4.5	4.5	4.5	5.4	4.3	4.3	4.3	4.3	4.3	3.5
1760.5	312.5	312.5	311	219	219	. 219	219	179	179	179	179	172	172	172	172	172	138.5
28	53	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

#### ALIGNMENTS

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MEDUM TYPE: Distacte COMPUTER: LBM Competible COMPUTER: LBM Competible OPERATING SYSTEM THE SYSTEM FAINTOWN BY WINDOWS VERSION 2.0 CURRENT APPLICATION UNMERR: US/08/674,887A RTILING DATE: 03-701-1996 RION REPLICATION NUMBER: 03-701-1996 APPLICATION NUMBE
                                                                                                                                                                                                                          APPLICANT: Reberison, Dan E.
PUDICANT: SOLVAI, Indialit APPLICANT: SOLVAI, Indialit APPLICANT: SOLVAI, Indialit APPLICANT ADIAS ANNERS: NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ATS & RICHARDSON P.C. STREET: 422 SEC
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ATTOANNY AGGRY INVORMATION:
NAME: Halle Ph.D., Lisa A.
REGISTRATION NUMBER: 38, 347
REFERENCE/DOCKET NUMBER: 09.015/002001
TREECOMMUNICATION INVORMATION:
TREEPHONE: 619/678-5099
INPORMATION FOR 880 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
                                                    Sequence 8, Application US/08674887A Patent No. 5939300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                     GENERAL INFORMATION:
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US-08-674-887A-8
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Gaps '0; ö Length 745; Indels DB 2; Query.Match 100.0%; Score 4002; Best Local Similarity 100.0%; Pred. No. 0; Matches 745; Conservative 0; Mismatches

US-08-674-887A-8

1 MENHKHSGSSTYNTINTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPN 60 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGAGAGTIPDAHDPSKSHAPFWLTTDLALRWDPDYEKISRRYYENPDEFADAFAKAWYKL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNK 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIKPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSND 660
                                                                                                                                                                     61 DPDFDYAEEFEKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAMHSAGTYRIGDG
                                                                                                                                                                                                                                                                                               181 KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNG
                                                                                                                                                                                                                                                                                                                 1 MENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPN
                                                                                                1 MENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWAPNMLNLGILRQHSSLSDPN
                                                                                                                                                                                                                        RGGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGF
                                                                                                                                                                                                                                              KPDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNK
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       DB 3; Length 745;
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100.0%; Score 4002;
100.0%; Pred. No. 0;
ive 0; Mismatches
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FFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCAD 720
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       SLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPK 360
                                                                                                              DGAGAGTIPDAHDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKL
                                                                                                                                                                                                                                                                                                                                                               601 YIKPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSND
                                                                                                                                                                                                                             THRDMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVST
                                                                                                                                                                                                                                                                                                                                    481 AWASASTFRNSDKRGGANGARIRLAPQRDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Resistant Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....recSSEE: Schwegman, Lundberg & Woessner STREET: 3500 IDS Center CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: COCKELIL, Franklin R.
APPLICANT: Kline, Bruce C.
APALICANT: Kline, Bruce C.
APALICANT: Mil. James R.
TITLE OF INVENTION: Detection of Isoniazid
TITLE OF INVENTION: of M. Tuberculosis
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WOCSSNEr, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 150.141US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    721 SEEKFVKDFVKAWAKVMDLDRFDLK 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEEKEVKDEVKAWAKVMDLDREDLK 745
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APPLICATION NUMBER: US/08/418,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) Sequence 7, Application US/08418782; Patent No. 5658733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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LENGTH: 740 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: MODELSON.
APPLICANT: SANDAL.
APPLICANT: APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 4002; Best Local Similarity 100.0%; Pred. No. 0; Matches 745; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: dialie Ph. D. Lisa A.
REGISTRATION NUMBER: 39.347
REPRESSOR MAMBER: 39.945/002001
TELECOMMUNICATION INFORMATION:
TELEPRONE: 619,676-6070
TELERA: 619,676-5070
TELERA: 619,676-5070
APPLICATION NUMBER: US/09/412,347 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/674,887
FILING DATE:
                                                                                                                                                                                           Sequence 8, Application US/09412347
Patent No. 6410290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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amino acid
GY: linear
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FRAGMENT TYPE: internal
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                                                                                                                                                                    US-09-412-347-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 TFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGK
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                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: WOSSONCY. MAITED D.
REGISTRATION NUMBER: 30,440
REFERENCE/ACKET NUMBER: 150.141US1
TELEPRAS: 612-39-031
TELEPRAS: 612-39-031
TELEPRAS: 612-39-3061
INFORMATION POR SED ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 740 amino acids
TIPE: amino acid acids
TOPE: amino acid acids
TOPE: alloar
                                                                                                                                                                                       US/08/418,782
                                                                   ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
         3500 IDS Center
                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-418-782-21
                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                          CLASSIFICATION: 435
                    CITY: Minneapolis
STATE: MN
                                                                                                                                                         SOFTWARE:
                                                       COUNTRY:
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                                                                                                                                                EGHPPITETTTGAASNG-CPVVGHMKYPVEGGG--NQDWWPNRLNLKVLHQNPAVADPMG 59
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                                                                                                                                                                                   62 PDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGR
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                                                                                      Gaps
                                                                                   Indels 10;
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APPLICANT: Kline Bruce C.
APPLICANT: Will, James R.
TITLE OF INVENTION: Defection of Isoniazid Resistant Strains
TITLE OF INVENTION: Of M. Tuberculosis
NORBER OF SEQUENCES: 22
NORBER OF SEQUENCES: 22
                                                     Length 740;
                                                63.6%; Score 2544; DB 1;
64.3%; Pred. No. 9.5e-222;
tive 88; Mismatches 168;
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DAQPKFVQDFVAAWDKVMNLDRFDVR 740
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Patent No. 5658733
GENERAL INFORMATION:
                                                                 Best Local Similarity 64.3%
Matches 480; Conservative
    protein
; MOLECULE TYPE:
US-08-418-782-7
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                                                Query Match
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ZIP: 55401 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk ATTORNEY/AGENT INFORMATION: TELEPHONE: 612-305-1226 US-08-852-219-7 COUNTRY: 099 362 g à g g 셤 g ò 셤 ò 셤 ð g ò 셤 ò ò à ö 60 AAFDYAAEVATIDVDALTRDIEEVWITSQPWWPADYGHYGPLFIRWAWHAAGTYRIHDGR 119 182 TFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGK 241 DFFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCA 719 PDFDYAEEFKKLDLAAVKKULAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGR 121 GGGCSCSCRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFK 181 3 EGHPPITETTGAASNG-CPVVGHMKYPVEGGG--NQDWWPNRLNLKVLHQNPAVADPMG 59 2 ENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPND Gaps 10; GENERAL INFORMATION:
APPLICANT: COCKRELL, FRANKLIN R.
APPLICANT: KLINE, BRUCE C.
APPLICANT: UBL., JAMES R.
TILLE OF INVENTION: DETECTION OF ISONIAZID RESISTANT STRAINS
TILLE OF INVENTION: OF W. TUBRROULOSIS Length 740; Indels MEDIUM TYPE: Ploppy disk
COMPUTER: IRM PC COMPALIAble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMEE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NAMER: US/08/228,662
FILLING DATE: 18-APR-1994
CLASSIPPICATION: 435 63.6%; Score 2544; DB 1; 64.3%; Pred. No. 9.5e-222; 11ve BB; Mismatches 168; CORRESPONDENCE ADDRESS:
ADDRESSE: SCHREMAN, LONDBERG & WOESSNER,
STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS TALEMENT OF THE TALE OF THE TA DSEEKFVKDFVKAWAKVMDLDRFDLK 745 DAQPKFVQDFVAAWDKVMNLDRFDVR 740 Sequence 7, Application US/08228662 Patent No. 5688639 ATTORNEY/AGENT INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 740 amino acids TYPE: amino acid STRANDEDNESS: single Ouery Match Best Local Similarity 64.3<sup>1</sup> Matches 480; Conservative COMPUTER READABLE FORM: MEDIUM TYPE: Floppy MOLECULE TYPE: peptide NUMBER OF SEQUENCES: STATE: MINNESOTA COUNTRY: USA linear 55402 TOPOLOGY: RESULT 6 US-08-228-662-7 US-08-228-662-7 296 9 959 720 62 122 120 900 g ф ò 윱 ð g à 셤 õ g à à

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GAGAGTIPDAH-DPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKL 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 NYIKPEHKVSABEMLVDRAQLLSLSAPEMTAIVGGMRVLGTNYDGSQHGVFTNKPGQLSN 659
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                                                                                                   242 PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAGIEEMS
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APPLICANT: Kilne Bruce C.
APPLICANT: Will Bruce C.
TITLE OF INVENTION: Defection of Isoniazid Resistant Strains
TITLE OF INVENTION: Of M. Tuberculosis
NUMBER OF SEQUENCES: 22
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT PAPLICATION DAYA:
APPLICATION NUMBER: 08/08/08/2119
FLING DAYE: 07-M8/1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUDRESSEE: Wueting, Reasch & Gebhardt, P.A. STREET: 119 NO. 5922575th Fourth Street, Ste. CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sandberg, Victoria A.
REGISTRATON UNDMER: 41.287
REFERENCE/DOCKET UNDMER: 230.0010130
TELECOMMUNICATION INFORMATION:
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715 DAQPKFVQDFVAAWDKVMNLDRFDVR 740
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Patent No. 5922575
GENERAL INFORMATION:
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APPLICANT: Kline, Bruce C.
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                                                                                                                                     COUNTRY:
                                                                                                           CITY: 1
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKD 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 AWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQ-QLARVLKTLEGIQEDFNQAQSDN 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 KAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFR 599
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                                                                                                                                                                                                                3 EGHPPITETTTGAASNG-CPVVGHMKYPVEGGG--NQDWWPNRLNLKVLHQNPAVADPMG 59
                                                                                                                                                                                      2 ENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPND 61
                                                                                                                                                                                                                                                                                              GGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFK
                                                                                                                                                               Gaps
                                                                                                                                                              Indels 10;
                                                                                                                                    Length 740;
                                                                                                                                Ouery Match 63.6%; Score 2544; DB 2;
Best Local Similarity 64.3%; Pred. No. 9,5e-222,
Metches 480; Conservative 88; Mismatches 168;
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Patent No. 5922575
GENERAL INFORMATION:
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 7:
                        SEQUENCE CHARACTERISTICS:
LENGTH: 740 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-852-219-7
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AFDYAAEVATIDVDALTRDIEEVWITSQPWWPADYGHYGPLFIRMAWHAAGTYRIHDGR 119 TFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGK 241 GAGAGTIPDAH-DPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKL 420 THRDMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVST 480 416 IHRDMGPVARYLGPLVPKQTLLMQDPVPAVSHDLVGEAEIASLKSQIRASGLTVSQLVST 475 62 PDFDYAEEFKKI.DLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGR 121 GGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFK 181 PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMS 301 LGWKNTYGTGHGADTITSGLEGAWTKTPTOWSNNFFENLFGYEWELTKSPAGAYQWKPKD 361 3 EQHPPITETITGAASNG-CPVVGHMKYPVEGGG--NQDWWPNRLNLKVLHQNPAVADPMG 59 2 ENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPND 10; APPLICANT: Uhl, James R. TITLE OF TWORMYN. Detection of Isoniazid Resistant Strains TITLE OF INVENTION: Of M. Tuberculosis 'NUMBER OF SEQUENCES: 22 Length 740; Query Match 63.6%; Score 2544; DB 2; Length 74 Best Local Stailarity 64.3%; Pred. no. 9,5e-22; Matches 189; Conservative 88; Mismatches 188; Indels Patentin Release #1.0, Version #1.25 CORRESPONDENCE ADDRESS: ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 5922575th Fourth Street, Ste. ATTORNEY/AGENT INFORMATION:
NAME: Sandberg, Victoria A.
REGISTRATION NUMBER: 41,287
REFRENCE/DOCKET NUMBER: 230,00010130 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,219
FILING DATE: U7-May-1997
CLASSIFICATION: 435 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS TELERAK: 612-305-1420
INCORATION FOR END ID NO: 21: SEQUENCE CHARACTERISTICS:
LENGTH: 740 anino acids
TYPE: amino acids TELECOMMUNICATION INFORMATION TELEPHONE: 612-305-1226 TOPOLOGY: linear MOLECULE TYPE: protein US-08-852-219-21 Minneapolis 셤

481 AWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQ-QLARVLKTLEGIQEDFNQAQSDN 539

Cockerill, Franklin R.

APPLICANT:

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TILE OF INVENTION: Nucleic Acid Probes, Sequences, and Methods
TILE OF INVENTION: for Detecting Mycobacterium Tuberculosis Resistant to Isoni
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett 6
ADDRESSER: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311
                                                                                                                                                                                                                                                                           HGADTITSGLEGAWTKTPTOWSNNFFENLFGYEWELTKSPAGAYOWKPKDGAGATIPDA 371
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                                                                                                                    132 APLNSWPDNANEDKARELEUPIKOKYGRKISWADEMILTGNVALETMGFKTFGFAGGRAD 191
    RETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTG
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APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart T.
APPLICANT: Young, Douglas B.
APPLICANT: Zhang, Ying
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STATE: DC
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                                                                                                                                   540 KAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFR
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APPLICANT: Benner, Madine
APPLICANT: Honore. Madine
APPLICANT: Telenti, Amalio
APPLICANT: Bodner, Thomas
APPLICANT: BODNER, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF ENVENTION: In Mycobacterium Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 726;
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ADDRESSE: Flinegan, Henderson, Farabow, Garrett
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
GURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: IZ-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 2421.5; DB 2;
; Pred. No. 1.2e-210;
78; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE, COCKET WHERE: 02356,0068-00000
TELECPHONE: (2021) 408-4400
TELEFRAM: (2021) 408-4400
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               DAQPKEVQDEVAAWDKVMNLDRFDVR 740
                                                                                                                                                                                                                                                       DSEEKFVKDFVKAWAKVMDLDRFDLK 745
                                                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/08313185
Petent No. 5551763
GENERAL INFORMATION:
APPLICANT: Heym, Reate
APPLICANT: Cole, Stewart
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STREET: 1300 I Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.5%;
Best Local Similarity 63.6%;
Matches 467; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
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TOPOLOGY: linear
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ZIP: 20005-3315

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551 AGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSA 610
                                                              EEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Young Douglas
APPLICANT: Young Douglas
APPLICANT: Zhang Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenit, Amalio
APPLICANT: Bodimer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
TITLE OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 726;
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ADDRESSE: Finangan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITE: 2006-3131
COMPUTER READABLE FORM:
WEDING TIPE: RIOPPY GISK
COMPUTER: TIM FO COMPOTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PALEDIELT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.5%; Score 2421.5; DB 3;
63.6%; Pred, No. 1.2e-210;
ive 78; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESIDENTATION NUMBER: 25,146
REPERBENCE/JOCKER NUMBER: 02356.0068-00000
TELECOMMUTICATION TREORMATION:
TELEPHONE: (202) 408-4000
TELEPHONE: (202) 408-4400
INTORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/082,614A
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APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49, Application US/09082614A Patent No. 6124098 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heym, Beate
Cole, Stewart
Young, Douglas
Zhang, Ying
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-082-614A-49
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 KLDYYGLKKDLKALLTESQPWWPADWGSYAGLFIRWAWHGAGTYRSIDGRGGARGQQRF 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 VWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 VWEPDLDVNWGDERAWLTHRHPEA - - LAKAPLGATEMGLIYVNPEGPDHSGEPLSAAAAI 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 VGADAITSGLEVVWTQTPTQWSNYFFENLFKXEWVQTRSPAGAIQFEAVD--APELIPDP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 HDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRY 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 FDPSKKRKPTMLVTDLTLRFDPEFEKISRRFLNDPQAFNEAFARAWFKLTHRDMGPKSRY 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 LGPEVPQEDLIWQDPIPD-VSHPLVDENDIEGLKAKILESGLTVSELVSTAWASASTFRN 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 SDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVL 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 YNTNTGGKCPFTGGSLKQSAGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.5%; Score 2421.5; DB 2; Length 726; 63.6%; Pred. No. 1.2e-210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
COMPUTER: IND OPPY disk
COMPUTER: IND COMPUTER
OPERATING SYSTEM: PC-COMPALIANG
OPERATING SYSTEM: PC-COS/MS-DG
CURRENT PAPLICATION DATA:
APPLICATION NOTHER: 05/08/450 ***
CLASSTRUCTON TO SAME OF THE OPEN OF THE OPEN OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 03495,0110-03000
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                             02-JUN-1995
                                                                                                                                                                                                                                                                                     FILMS DATE: 37-HAY-1992
PRICH APPLICATION DATE:
APPLICATION NAME:
                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/875,940 FILING DATE: 30-APR-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/029,655
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 726 amino acids
amino acid
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Matches 467; Conservative
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                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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428 KVRYLGPEVPQEDLIWQDPIPDVSHPLVD--ENDIEGLKAKILESGLTVSELVSTAWASA 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 ADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVOMGLIYVNPEGPNGKPDPIAAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 EDVWEPDLDVNWGDEKAWLTHRHPEA - LAKAPLGATEMDLIYVTPEGPNHSGEPLSAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 TYNTINIGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 RFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFKTFGFAGGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.9%; Score 2397; DB 2; Length 7 62.8%; Pred. No. 2e-208; ive 82; Mismatches 171; Indels
                                                                                                                                                                                                       SOFTWARE: Patentin Release #10, Version #1.25
CURRENT APPLICATION DATA: APPLICATION NOMER: US/08/313,185
FILING DATE: IZ-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02356.0068-00000
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY ZEGNT INFORMATION:
AMARI: Meyers Renneth 3.
REGISTRATION WUMBER: 0.5.146
REGISTRATION WUMBER: 0.35.46
RELECOMMUNICATION INFORMATION:
INFORMATION 10.9 408-4000
INFORMATION POR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 729 amino acids
TYPE: amino acid
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Matches 465; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         IGPEVPQEDLIWQDPIPD-VSHPLVDENDIEGLKAKILESGLTVSELVSTAWASASTFRN 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVL 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSA 610
                                                                                                        KLDLAAVKKDLAALMIDSQDWWPADYGHYGPFFIRMAWHSAGIYRIGDGRGGGGGGGGGR 131
                                                                                                                                                                                                                                                                          APLNSWPDNVSLDKARRLLWPIKQKYGQKISWADLFILAGNVALENSGFRTFGFGAGRED 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 HGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGGTIPDA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDPSKSHAPFMLTTDLALRMDPDFEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRY 431
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                                                                                                                                                                                                                                         APLINSWPDNANLDRARLLLMPIKQKYGRKISWADIMILTGNVALETMGFKTFGFAGGRAD 191
SELLIDKAQQLTLTAPEMTALVGGMRVLGGNFDGSKNGVFTDRVCVLSNDFFVNLLDMRY
                                                                                                                                                                                                                                                                                                                                                                              VWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDI
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APPLICANT: Wing, Douglas
APPLICANT: Wing, Ting
APPLICANT: Petert, Mallo
APPLICANT: Petert, Mall
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Patent No. 5851763
GENERAL INFORMATION:
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STREET: 1300 I Street, N.W.
CITY: Washington
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Cole, Stewart
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71 KKLD-LAAVKKDLAALMIDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGSGSQ 129
                                                         130 RFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFKTFGFAGGR 189
                                                                                                                                                                                                                                                    190 ADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAAR 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 TGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGAGTIP 369
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APPLICANT: Poung, Jouglas
APPLICANT: Poung, Tung, APPLICANT: Rapid Detection of Antibiotic Resistance TITLE OF INVENTION: In Mycobacterium Tuberculosis
NORBEN OF SEQUENCES: 66
NORBEN OF SEQUENCES: 67
NORBEN OF SEQUENCES: 
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APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
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US-09-082-614A-50
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DVSTTESLLIDKAQQLTLTAPEMTVLVGGMRVLGTNFDGSQNGVFTDRPGVLSTDFFANL 649
                                                                                                LDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKF 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: WESTER, Kenneth J.
REGISTRATION NUMBER: 25,146
FERENCE/POCKET NUMBER: 03495.0110-03000
TELECHMONICATION INTERNATION:
TELECHMONICATION INTERNATION:
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FILING DATE: 025-1995
CLASSIFICATION: 5 M. 1995
RICH APPLICATION DATE: 07/075,940
FILING DATE: 30-APPL-1992
PRIOR APPLICATION NAME: 1897
PRIOR APPLICATION NAME: 1897
FILING DATE: 37-MY-1992
FILING DATE: 1897
FILING DATE: 11-MY-1992
APPLICATION NUMBER: 1898
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                                                                                                                                                                                                                                                                              726 VKDFVKAWAKVMDLDRFDLK 745
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Patent No. 5871912
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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Sequence 8115, Application US/09328352
Patent No. 6562398
Patent No. 6562398
Patent No. 6562398
TILLE OF INVERTIONS:
TILLE OF INVERTIONS: BACAMAINI FOR DIAGNOSTICS AND THERADEUTICS
TILLE OF INVERTIONS: BACAMAINI FOR DIAGNOSTICS AND THERADEUTICS
TILLE OF INVERTIONS: BACAMAINI FOR DIAGNOSTICS AND THERADEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SED ID NOS: 8252
SED ID NOS: 8252
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                                                              74 ALKADIKNVLTDSQDWWPADWGNYTGLFIRLAWHAAGTYRMGDGRGGAGRGQQRFAPLNS 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMAMNDEETVALIAGGHTFCKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTGHGADT 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHAPFMLTTDLALAMOPDIEKISRRYYENPDEFADAFAKAWYKLTHROMGPKVRYLGPEV
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       590 DVSTTESLLIDKAQQLTLTAPEMTVLVGGMRVLGTNFDGSQNGVFTDKPGVLSTDFFANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 KCPFTGGSLKQ---SAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKKLDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGGGGGGGGFAPLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDIRETFG
                                         LDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKF
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                                                                                                                                       710 VKDFVAAWVKVMNLDRFDLQ 729
                                                                                                                  726 VKDFVKAWAKVMDLDRFDLK 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Acinetobacter baumannii
US-09-328-352-8115
                                                                                                                                                                                                                                US-09-328-352-8115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGGTIP 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAHDPSKSHA -- PFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGP 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVRYLGPEVPQEDLIWQDPIPDVSHPLVD--ENDIEGLKAKILESGLTVSELVSTAWASA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLA 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 THNTLSTGKCPFHQGGHDRSAGAGTASRDWWPNQLRVDLLNQHSNRSNPLGEDFDYRKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 ADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 2397; DB 3; Length 7; Pred. No. 2e-208; 82; Mismatches 171; Indels
                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    02356.0068-00000
                                                                                             APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 08/313,185
FILING DATE: 12-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          NAME: Meyers Kenneth J.
REGISTRATION NUMBER: 25,146
REPRENCE/POCKER NUMBER: 0236
TELECOMMUNICATION INCORMATION:
FELEPHONE: (202) 408-4400
INFORMATION FOR SEO ID NO: 50;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.9%;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 729 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 62.83
Matches 465; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) MOLECULE 11F1
US-09-082-614A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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0y	617	617 RAQLISISAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTKWRASD 676	
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qq	298	598 KAQQLTLTAPELTALIGGLRVLGTNWDGSQHGVFTQQVGVLSTDFFTNLLDMSNVWAPVD 657	657
Qy	677	677 ESDKVPEGRDFKTGEVKMSCTRVDLIFGSNSELRALAEVYGCADSEEKFVKDFVKAMAKV 736	736
qq	658	658 SISEVPEGKDRKSGTVKFTATRNDLVFGSNSILRALAEVYAQADGKEKFVQDFVAAAWTKV 717	717
δλ	737	737 MDLDRFDL 744	
QQ	718	718 MILDRFDL 725	

Search completed: October 7, 2003, 19:47:37 Job time : 24.8825 secs

us-09-884-889-8.rapb

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

US-09-884-889-8 4002

October 7, 2003, 19:45:48; Search time 48:241 Seconds (Withbot alignmenta) 2443:330 Million cell updates/sec

Run on:

Perfect score:

1 MENHKHSGSSTYNTNTGGKC.....VKDFVKAWAKVMDLDRFDLK 745 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

587654 Total number of hits satisfying chosen parameters:

587654 seqs, 158212981 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_AA:\*

1. cga12\_cfptodata/Tpubpaa/R017\_PUBCOMB.pep:\*

2. cga12\_cfptodata/Tpubpaa/R017\_NBW\_PUB.pep:\*

3. cga12\_cfptodata/Tpubpaa/R016\_NBW\_PUB.pep:\*

4. cga12\_cfptodata/Tpubpaa/R016\_NBW\_PUB.pep:\*

5. cga12\_cfptodata/Tpubpaa/R016\_NBW\_PUB.pep:\*

5. cga12\_cfptodata/Tpubpaa/R017\_NBW\_PUB.pep:\*

6. cga12\_cfptodata/Tpubpaa/R018\_NBW\_PUB.pep:\*

9. cga12\_cfptodata/Tpubpaa/R018\_PUBCOMB.pep:\*

10. cga12\_cfptodata/Tpubpaa/R018\_PUBCOMB.pep:\*

11. cga12\_cfptodata/Tpubpaa/R019\_PUBCOMB.pep:\*

12. cga12\_cfptodata/Tpubpaa/R019\_PUBCOMB.pep:\*

13. cga12\_cfptodata/Tpubpaa/R019\_PUBCOMB.pep:\*

14. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

15. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

16. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

17. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

18. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

19. cga2\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

11. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

12. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

13. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

14. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\*

16. cga12\_cfptodata/Tpubpaa/R010\_PUBCOMB.pep:\* Database :

### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 67, Appl Sequence 2, Appli Sequence 47, Appl Sequence 3135, Ap	Sequence 10145, A Sequence 5962, Ap Sequence 12011, A Sequence 9789, Ap	Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7036, Ap Sequence 7965, Ap	14403 3481, 196, 9681, 111, 2	Sequence 18, App Sequence 11, App Sequence 12898, A Sequence 2, Appli Sequence 10432, A Sequence 11464, Appli Sequence 11464, A
US-10-193-764-67 US-09-817-514A-2 US-10-242-056-47 US-10-128-714-3135 US-10-128-714-8135	<b>D</b>	US-10-244-B21- US-10-013-173- US-10-150-762- US-10-032-585- US-10-156-761-		
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1477 2516 2516 2516 2192 2209	1247 904 493 1281	431 431 431 1097 7746	720 918 929 7426 7426	811 610 622 1248 1536 366 855 855
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#### ALIGNMENTS

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	Gaps	SSLSDP	TYRIGD        TYRIGD
	745;	ILROH IIIII ILROH	WHSAG       WHSAG
	Length 745; Indels 0;	MENHKHSGSSTYMTNTGGKCPPTGGSLKQSAGGTKNRDWAPMLMLDILRQUSSLSDPN 	DEDEDYARREKKIDLAAVKKOLAALWTDSQDWIPADYGHYGPFFIRMAKHSAGTVRIGG 
	DB 10;	NRDW 	YGHY 
		366TF	WPAI             WPAI
7 7 4 4 7 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4002; No. (atche	KOSAC           KOSAC	AGOSG 1111
884, 2,34 11,84 4,88	Score 4002; Pred. No. 0; 0; Mismatches	GGSL	ALMI ALMI
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Sequence 8, Application US/09884899 Factent No. US2002102680A1 GENERAL INCREMATION APPLICANT: DIVERSA CORPORATION APPLICANT: ROBERFOOK, Dan APPLICANT: ROBERFOOK, Dan APPLICANT: ADBIEKEN, RODGET TITLE OF INVENTION: CAPALSES FILE NEFRENCE: 100 100 100 100 100 100 100 100 100 10	Query Match Best Local Similarity Matches 745; Conser		
Sequence 8 A General No. 10 CENERAL	Que Bes Mat	60 O	Oy Dp

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Query Best I Matche	δŏ	윰	δλ	<b>a</b>	δ	QG .	òé	3 &	. a	δδ	ପ୍ଧ	δλ	qq	δō	qq	ďδ	dg.	δ	q	δδ	qq	ò	a a	λο	90		RESULT 3	; Sequent	_		; FILE	CORRECT	PRIOR
121 RGGGSGSGRPAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGF 180 			241 KPDPIAAARDIRETFGRAAMNDEETVALIAGGHFGKTHGAADAEKYVGREPAAAGIEEM 300	241 KPDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKTVGREPAAAGIEEW 300	301 SLGWKNTYGTGHGADTITSGLEGAMTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPK 360	301 SLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPK 360	361 DGAGAGTIPDAHDPSKSHAPPMLTTDLALRUDPDYEKISRRYYENPDEFADAFAKAWYKL 420		441 HROWGEKVRYGEPPOEDLINODPIPDVSHELVDENDIEGIEGAKTILESGLIVSELVST 480 					601 YIRPEHKVSAEEMIVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNRPGQLSND 660		661 FFVMLLDLMTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCAD 720		721 SEEKFVKDFVKAWAKVMDLDRFDLK 745			9-68	Sequence 6, Application US/09884889 Patent No. US20020102680Al	GENERAL INFORMATION: APPLICANT: DIVERSA CORPORATION		APPLICANT: ADMITMA, MALINATURE APPLICANT: ADMITMAN, ADMITMAN OF THE APPLICANT OF THE APPLIC	FILE REFERENCE: DIVERLING. CALABASES CHRENCE DIVERLING. CALABASES CHRENCE APPLICATION WINESES. IT AND ADDA	FILING DATE: 2001-06-19	FRION REFLICATION NUMBER: US US/412,347 PRION DATE: 1999-10-05	PRIOR PILICATION NUMBER: US 08/951,844 PRIOR FILING DATE: 1997-10-16	PRIOR APPLICATION NUMBER: US 08/674,887 PRIOR FILING DATE: 1996-07-03	r Sel ID NOS: 8 : Patentin Version 3.0 6	753 RT	ORGANISH: Alcaligenes (Deleya) aquamarinus S-09-884-889-6
0y 1		Db 1	Oy 2	Dp 5	oy 3	Dp 3			φ <del>φ</del>	Oy 4	QQ qq	Oy S	Dp 2'	Qy 6(	)9 . qa	oy 60	op qu	0y 7:	7;		RESULT 2 US-09-884-889-6	Sequence (		APPLICANT:						PRIOR APP	S	LENGTH: 753 TYPE: PRT	ORGANISA IS-09-884-88

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78 VKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGSGSQRFAPLNSW 137
                                                                                                                                                                                                   PDNANLDKARLLLWPIKQKYGRXISWADLMILTGNVALETMGFKTFGFAGGRADVWEPEE 197
                                                                                                                                                                                                                                                                                             252 RETFGRMANNDEETVALLAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 HGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGAGTIPDA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 KASINAYISGIEGAWIINPIKEDMGYFDLIFGYNWELKKSPAGAHHWEPIDIKKENKPVDA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 HDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRY 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 LGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVSTAWASASTFRNS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIOEDFNQAQSDNKAVSLADLIVLA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAE 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTK 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              672 WRASDESDKVPEGRDFKTGEVKRSCTRVDLIFGSNSELRALAEVTGCADSREKFVKDFVK 731
681 WR--PVGSNAZIEDRITGARVATARSVDVPGSNSELRSYAEVTADNGSKRVREVA
682 WR--PVGSNAZIEDRITGARVATARSVPUVPGSNSELRSYAEVTADNGSKRVREVA
                                                                                             77
                                                                                                                  JICART: Takaba, Tessuko

E. OF INVERTION: Percentanal Ascorbate Percentanse Gene Induced by High
E. OF INVERTION: Percentanse Ascorbate Percentanse Gene Induced by High
E. OF INVERTION: Temperature Stress and a Trangenete Plant Exhibiting
E. OF INVERTION: Thermocolerance
E. OF APLICATION MORRER: US 0.09/870,501
ENT FALING DATE: 2001-06-01
ENT FILING DATE: 2001-06-01
ENT FILING DATE: 2001-06-01
ENT FILING DATE: 2001-06-01
                                                                                   18 GRCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFRKLDLAA
57.2%; Score 2290.5; DB 10; Length 753;
59.1%; Pred. No. 2.1e-200;
11ve 92; Mismatches 183; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nce 1, Application US/09870501
t No. US20020100081A1
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SOFTWARE: Patentin version 3.1
                  Local Similarity 59.18 es 433; Conservative
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   Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 DFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 GGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADIMILTGNVALETMGFKT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 WKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGA 363
                                                                                                                                                                                    111 IVFVPGRKD----SNVCPKEGRL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 LGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKD 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 ------RSGFDGPWTQEPLNFDNSYFVR-----ELLK----- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 GAGAGTIPDAHDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| :| | ::| :| :| :| :| :| :| :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
                                                                                                                                                                                                                                                                         364 GAGTIPDAHDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLT 421
                                                                                                                                                                                                                                                                                                                                              203 --------FQLPSDKALLSDPVFRPLVEKYAADEKAFFDDYKEAHLKLS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wathalie Verbruggen
TITE OF INVENTION: Genes Uncload in Tolerance to Environmental Stress
FILE REPREBENCE: ON JUNG SINCHALL
CURRENT PELICATION NUBBE: US_/10/342,24
CURRENT PELICATION NUBBE: US_/10/342,154
PRIOR APPLICATION NUBBE: US_/09/762,154
PRIOR PELICATION NUBBE: US_/09/762,154
PRIOR PELICATION NUBBE: US_/09/762,164
PRIOR FILING UNBER: US_/08/604
NUBBE: OS_D ID NOS: 123
SOFTWARE: PSELENG FOR WINGOWS VERSION 4.0
LENGTH: 307
LENGTH: 307
LENGTH: 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 287;
          Best Local Similarity 23.0%; Pred. No. 2e-12;
Matches 84; Conservative 46; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%; Score 229.5; DB 23.0%; Pred. No. 2e-12;
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Patent No. US/20/2014/2018

PAPPLICANT: Lerchl, Jens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/10342224
Publication No. US20030162294A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ELGFNP 246
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US-10-342-224-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 PLGAVQMGLIYVNPEGPNGK-PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 -----SSVCPR--EGRLPDAKKGAPHLRDIFYRWGLTDKDIVAL-SGGHSLGKAHP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 AADAEKYVGREPAAAGIEEMSLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENI, 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 E----RSGFDGAWTRDPLKFDNSYF--- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 FGYEWELTKSPAGAYQWKPKDGAGAGTIPDAHDPSKSHAPFMLTTDLALRMDPDYEKISR 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 GSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFKTFG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 FHPGREDKPQPP----PEG--RLPDA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 IAAARDIRETFGR-MAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 FAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 SWADIMILIGNVALETMGFKTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELEN
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                                                                                                                                                                                                                                                                                                         95; Indels 115;
                                                                                                                                                                                                                                    Length 291;
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GENERAL INFORMATION: CALL
TITLE OF INVESTION: Make Defense-Inducible Genes and Their
TITLE OF INVESTION: Make Defense-Inducible Genes and Their
TITLE OF INVESTION: Make TO STATE OF TOWN WORKER: US/10/027,559
CURRENT FILLING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 003-10-23
PRIOR FILLING DATE: 2006-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 RYYENPDEFADAFAKAWYKLTHRDMGPKVRYLGPEVPQEDL 441
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                                                                                                                                                                                                                               ch 6.8%; Score 273.5; DB 10;
1 Similarity 27.0%; Pred. No. 1.9e-16;
92; Conservative 39; Mismatches 95; 1
                                                                                                               ; ORGANISM: Hordeum vulgare L. Haruna-nijyo US-09-870-501-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 250
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SEQ ID NO 1
LENGTH: 291
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Best Local
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Sequence #481. Application US/J0128714
PUBLICATION TO 102703011013A1
PUBLICATE THE PROPERTY OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                      209 DVWK-----GTLTHHA--ETPADOPTELTVPLALYCRSSLAKDLDAVRLFTETKQGFDWY 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 PADYGHYGPF-----FIRMAWHSAGTYRIGDGRGGGSGSQ-RFAPLNSWPDNAN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 HRNFGVAYPFGKYDQIFVPEFNAGAMENAGAVTIRDEYVFASKATRKRYE----- 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 LDKARLLLWPIKQK-YGRKIS---WADLMILTGNVALETMGFKTFGFAGGRADVWEPEED 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 TAWVIFANVEKSW----AYQQDQ------390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 -----WELTKSPAGAYQWKPKDGAGATIPDAHDPSKSHAPFMLTTD---- 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 558 KAAKDAGHEVQVPFNPGRADATAEQTDVEAFE---ALEPAAD----GFRNYIKPEHKVSA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GLTVDPDLRWWALTALIARGDIEAVEDAIAAELSRDNSSASFLASLRAGAAVNT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                611 EEMLVDRAQLLSLSAPEMTALVGGM-----RVLGTNYDGSQH------GV 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 VYW----GAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDIRET 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  498 ngarirlapokdwevnnpoglarylktlegiqedfnqaqsdnkaysladliylagcagye 557
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                                                                                                                                                                                                                                                                                                                               39 DWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKKLDLAAVKKDLAA--LAMTDSQ---DWW 93
                                                                                                                                                                                                                                             Gapa
                                                                                                                                               Query Match

3.09; Score 111; DB 10; Longth 867;
Best Local Similarity 20.08; Pred. No. 0.097;
Matches 152; Conservative 94; Mismatches 771; Indels 242;
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            ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6164
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APPLICANT COLIAL RETRO
APPLICANT TOTOLA HARUIER
APPLICANT TOTOLA HARUIER
APPLICANT TOTESHI NOKO
APPLICANT SEROH, MASTO
APPLICANT SEROH, SANO
FILE OF INVENTION ROVEL POLYNUCLEOTIDES
FILE REPRENCE: 249-115
CURRENT APPLICATION RUMBER: 05/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR PAILLANTON WARREN: 19 99/717484
PRIOR PAILLANTON WARREN: 19 00/7189162
PRIOR PAPLICATION WARREN: 19 00/7189188
PRIOR PAPLICATION WARREN: 19 00/71809188
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PRIOR PAPLICATION WARREN: 19 00/71809188
PRIOR PRIOR PRIOR WARNEN: 10 00/71809188
SOFTHANTO 18 00/71809188
TARKEN: 877
TIPE: PRIOR WARREN: 10 00/71809188
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Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  Duwenig, Elke
Schmidt, Ralf-Michael
                                                                                                                                         Cirpus, Petra
Bischoff, Friedrich
Frank, Markus
Freund, Annette
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
Renz, Andreas
Ehrhardt, Thomas
Reindl, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Conservative
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Best Local Similarity
Matches 54; Conserv
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67 AEEFKKLDLA---AVKKDLAALMTDSQDWW-----PADYGHYGPFFIRMA-WHSA 112 113 GIYRIGDGRGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKOKYGRKIS------ 162 122 ADY-----RAAAANITTRLA-----TRYAEHPALALWHVHNEYGVPVSACYCESCAAH 169 163 ---WADLMILTGNVALETMGFKTFG--FAG-------GRA---------- 190 | : | | : | | | 229 | 170 FRRWLIDIYGTIDALNEAWGTAFWGORYAGFDQINPPRLIPIYGNPGQALDHKRFADAIM 229 191 -DVWEPEEDVY-----EGDREL 219 ENPLGAVQMG------LIYVNPEGPNGKPDPIAAARDIRETFGRMAMNDEETVALI 269 | | : | | | 111 | 11 | 120 | 120 VNLAMAADLTRSVASGAPWILIEHSTSGVNWQPHNPAKAP-----GQMARNSLAHVARG 343 ACCHTFCK-THCAADAEKYVGREPAAGIEEMSLGWRNTYGTGHGADTITSGLEGAWTKT 328 101 DVAVLWDWQSWWAQNL-------428 PT----QWSNNFFENLFGYEWELTKSPAGAYQWRPKDGAGAGTIPDAHDPSKSHAPFMLT 384 5 TPKGLTRIAFGGDYNPEQWPETVWQEDVRLMREAGVTWVSVGIFSW--ALLEPSPGAYDF 62 23 TGGSLKQSAGGGTKNRDWWP-------NMLNLGILRQHSSLSDPNDPDFDY 66 Ouery Match
2.9%; Score 117; DB 15; Length 673;
Best Local Similarity 18:9%, Pred. No. 0.15;
Matches 129; Conservative 75; Mismatches 247; Indels 230; Gaps 220 270 셤 à g ò 셤 ò 셤 á a ò g ò 셤 ö 용 433 548 130 RFAPLN-----SWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGF 180 238 PNGKPDP------IAAARDIRETEGRMAMNDEETVALIAGGHTFGKTH 279 86 PDGTKIPGKLRLFSIGYSTAVTEWNLEQGRPMRHSSGNYG-----EIWCIAAQPRWQATK 140 280 GAADAE-----KYVGREPAAAGIEEMSLGWKNTYG--------TG 311 141 RGKDGKPLPPAEGEYTGQH-LAAGCADGSIVILSTADGDLKFLRIMRPSTKRARVLSVTF 199 312 HGADTITSGLEGAWIKTPTQWSNNFFENLFGYEWELTKSPAGAYQ----WKPK----- 360 361 --- DGAGAGTIPDAHDPS---KSHAPFMLTTDLALRMDPD-----YEKISRRYYENPDE 408 315 KGEKKGR-WAEVMHRRYHTHDVKTFAVYETRDISIVVSGGPDASPVVLPLREFGKEHHRK 373 434 ----PEVPQ-------EDLIWQDPIPDVSH-PLVDENDIEGLKAKIL---- 468 129 IQGEENITSAMISADGKILIVATVSAVKVFSVRRRKSDERGTLRITKIDVPAAFSKDGAR 488 502 -IRLAPQKDW------KTLEGI 528 200 ONRNTIVAGYADSSIRLFDLRSGQLLRTI----SLGKGPAGGPKELLVWSVKCLPDGTI 254 581 EQTDVEAFEALEPAADG----FRNYIKPEHKVSAEEMLVD-----RAQLLSLSAPEMT 629 181 KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYV -- NPE-G ---ESGLTVSEL------GANGAR 529 QEDFNQA-----QSDNKAVSLADLIVLAGC--AGVEKAAKDAGHEVQVPFNPGRADATA 7 RFVPYNPQAINALSFSHPPSAEL------AGRGVPTLRLAI------42 ---GRANGDIEIWNPMRGA-WFQETVMRGGK----DRSIE------GLAWTLDPPEAG 409 FADAFAKAWYKLTHR-----RYLG-----489 AVSISPDSRWLCVVRPDSAIYLARVMPASSPQDKPQILPQLVKLDRATRHTRHEKASHGS Query Match
3.0%; Score 121; DB 15; Length 976;
Best Local Similarity 19.2%; Pred. No. 0.12;
Matches 160; Conservative 99; Mismatches 255; Indels 318; Gaps CURREAT APPLICATION NUMBER: US/10/128,714
CURREAT FILICATION NUMBER: US/02/04/23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FLIKEN DAME: 2001-04-23
PRIOR FLIKEN DAME: 2001-04-27
PRIOR FLIKEN DAME: 2001-04-27
PRIOR FLIKEN DAME: 2001-04-27
PRIOR PLIKEN DAME: 2001-04-29
PRIOR PRIOR DAME: 2001-05-09
PRIOR PRIOR DAME: 2001-05-09
PRIOR PRIOR DAME: 2001-05-09
PRIOR FLIKEN DAME: 2001-07-09
SEQUENCE PRIOR DAME: 2001-07-07-09
SEQUENCE PRIOR DAME: 2001-07-07-07-09
SEQUENCE PRIOR DAME: 2001-07-07-09
SEQUENCE PRIOR DAME: 2001-07-07-07-07-07-07-07-09
SEQUENCE PRIOR DAME: 2001-07-07-07-07-07-07-07-07-07-07-07-07-0 ; ORGANISM: Aspergillus fumigatus US-10-128-714-8481 FILE REFERENCE: 10182-018-999 469 605 요 요 q 엄 셤 a ð à q ð à à ŏ ò à g ò g ò g à g

31;

385 IDLALRMDPDYEKISRRY----YENPDEFADAF----AKAWYKLT-----HRDMGP 427

ογ	630 ALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTKW 672
qq	662 QISLRGESRLMALTSEHQLVEFDTLEGKLSDWSRRNPKAYLPEGFKGVKDRAMGCLW 718
δλ	673 RASDESDKVFEGRDFKTGEVKW-SGTRVDLIFGSNSELRALAEVYGCADSEE 723
ФQ	719 DLSESRDRLWLYGTSWLMWFDLNQDFPSSEEMKEAADGHE 758
RESULT	on.
US-10-1	US-10-156-761-8864
; Sedue	Sequence 8864, Application US/10156761
: Publ	Publication No. US20030119018A1
, GENE	GENERAL INFORMATION:
; APPI	APPLICANT: OMURA, SATOSHI
; APPI	APPLICANT: IKEDA, HARUO
; APPI	APPLICANT: ISHIKAWA, JUN
; APPI	APPLICANT: HORIKAWA, HIROSHI
; APPI	APPLICANT: SHIBA, TADAYOSHI
; APPI	
; APPI	APPLICANT: HATTORI, MASAHIRA
TIL :	TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE	FILE REFERENCE: 249-262
, CURI	CURRENT APPLICATION NUMBER: US/10/156,761
, CUR	CURRENT FILING DATE: 2002-05-29
; PRIC	PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIC	PRIOR FILING DATE: 2001-05-30
; PRIC	PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIC	OR FILING DATE: 2001-08-02
; NUM	NUMBER OF SEQ ID NOS: 15109
; SEQ :	ID NO 8864
Ē.	LENGTH: 673
; TYI	TYPE: PRT
, ORC	ORGANISM: Streptomyces avermitilis
-0T-SD	US-10-156-761-8864

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APPLICANT: RICKe, DAZTEL]
TITLE OF INVENTIOR: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REPERBACE: 70030-W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 -----GNVSVAQETNGNLPPPSANVAQLNQMFGAKGLTQAEMYAL-SGAHTIGVSHC 204
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CORRENT PILING DATE: 2002-09-26
PRIOR PILING DATE: 2002-09-36
PRIOR PILING DATE: 2002-04-30
PRIOR PILING DATE: 2002-04-30
PRIOR PILING DATE: 2002-03-370
PRIOR PILING DATE: 2002-03-377
PRIOR FILING DATE: 2002-03-577
PRIOR FILING DATE: 2001-09-26
SOUTHARE: PACENTIA'S NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
SOUTHARE: PACENTIA'S 1201-09-26
SOUTHARE: PACENTIA'S 1201-09-26
SOUTHARE: PACENTIA'S 1201-09-26
SOUTHARE: PACENTIA'S 1201-09-26
SOUTHARE: PACENTIA'S 131
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Best Local Similarity 20.4%; Pred. No. 0.11;
Matches 55; Conservative 26; Mismatches
    281 ADQTTAAQVVGYTNNPDSFQTDFAAAMVKM 310
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Publication No. US20030119018A1
APPLICANT: OMPON. SNYSHI
APPLICANT: OMPON. SNYSHI
APPLICANT: UNEDA, HARUO
APPLICANT: HKEDA, HARUO
APPLICANT: HORKRAMA, HIROSHI
APPLICANT: HORKRAMA, HIROSHI
                                                                                                                                                                           ; Sequence 360, Application US/10259165; Publication No. US20030135888al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Glazebrook, Jane
Goff, Stephen A.
Katadiri, Fumiyaki
Kreps, Joel
Moughamer, Todd
Provart, Nicholas
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Cooper, Bret
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Chang, Hur-song
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APPLICANT: K.C.D.S. JOE FULL 1864.
APPLICANT: POUGHER: TOOL APPLICANT POUGHER: TOOL APPLICANT POUGHER: TOOL APPLICANT POUGHER: TOOL APPLICANT: RICHARD TO GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING THIR STRENKE: 1003-09-97.
THILE OF INVESTION NOTION NOTION NOTION NOTION TO STRENKE: 1003-09-97.
BRIGH REPLICATION NOTION NOTION
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                                                                                                                                                                      484 TLVVSYFSGIVDEHDAVHDGPYPGAL ----- RDVLGLIVEEFSPLLKDDRIRVTGPDGS 537
                                                                                                                                                                                                                                    476 ELVSTAWA-----SASTFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLE 526
                                                                                                                                                                                                                                                                                                           ----TRLTAQ 590
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2.8%; Score 113; DB 12; Length 331; Bett Local Similarity 20.4%; Pred: No. 0.11;
Metches 55; Conservative 26; Mismatches 97; Indels 9
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
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Publication No. US20030135888A1
GENERAL INFORMATION:
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Chang, Hur-song
Briggs, Steven P.
Cooper, Bret
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Goff, Stephen A.
Katagiri, Fumiyak
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740 RVEIRRPHGNDIEIRAAGAAKDAPYVRSLKVDGRTSDRSWLPASFVRD----GGRLDYTL 795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARVGSGRGYLNSGYIANRKADGSWYTGFTPAT-GNGFVEGTAAQYTWWVQHNPAGLFAAM 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 LGAVGVGGGTAE----DRTTFYTALYHALLHPNVISDADRRYRGSDDKVHVVGRGHRAQY 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 HYGPFFIRMAWHSAGTYR-----IGDGRGG-----GGSGSQRFAPLNSW 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------PVNVKVG--ISYVSQAGAEANLAVENPRGRSFEAVRDAARRAWRER 333
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.8%; Score 112.5; DB 15; Length 1104; Best Local Similarity 18.7%; Pred. No. 0.85; Matches 136; Conservative 68; Mismatches 256; Indels 267; Gaps
         APPLICANT: HATTOR, MASALINA
APPLICANT: HATTOR, MASALINA
TITLE OF INVERTION: WOEE POLINUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FLILKS DATE: 2002-05-29
PRIOR PELLING DATE: 2002-05-39
PRIOR PELLING DATE: 2001-05-30
PRIOR APPLICANTON WINBER: JP 2001-272697
PRIOR APPLICANTON WINBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 390 D NOS: 15109
LENGTH: 1104
                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9790
SAKAKI, YOSHIYUKI
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387 LALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRYLGPEVPQEDLIWQDP 446 58 DPNDPDFDYAEEFKKLDLAAVKKDLAALMT------DSQDWWPADYGHYGPFFI 105 92 NIADADINWAG--RQLRLPRALPGLAGTVTRRANVPHRFALNDTND-----GYTGPYH- 142 106 RMAWHSAGTYRIGDGRGGGGGGGGGGGGGGGGRPLNSWPDNANLDKARLLLWPIKQKYGRKISWAD 165 166 IMILIGNVALETMGFKTFGFAGGRADVW--EPEEDVYWGAE-----TEWLGDKRYE 214 300 ----MSLGWKN-----TYGTGHGADTITSGL------EGAWTKTPTQWSNNFFEN 339 340 LFGYEWEL-----TKSPAGAYQ-WKPKDGA---GAGTIPDAHDPSKSHAPFMLTTD 386 445 LAWRE-----RYGGRD-PHAEAAW--- 477 447 IPDVSHPLVDENDIEGLKAKILESGLTVSELVSTAWASASTFRNSDKRGGANGARIRLAP 506 162 VLVQTGADALHHRVFQEFGYTDEELRKWIPGPAHQPWWLLQNLSAFPDPVSQQLLDARAA 221 5 KHSGSSTYNTNTGGKCPF--TGGSLKQSAGGGT----KNRDWWPNMLNLGILRQHSSLS 57 215 GDRELENPLGAVQMGLIYVNPEG--PNGKPDPIAAARDI---------RETF 222 LGRRIANRLRELGMTPVFPGYFGTVPPGFADRNAGAHTVPQGTWMGFARPDWLDPRTEHF 256 GRMA-----MNDEETVALIAGGHTFGKT----HGAADAEKYVGREPAAAGIEE-----282 TRVAAAFYRIQDE----MFGGASTRYKNDLLHEGGSPGDVPVG--DAAKGVERALRAAHP 336 GAVWVILGWOHNPPRAIVDAVDKDRMLVVDGLCDRFPKVTDREADWHGTP-----Y DB 15; Length 728; Indels 252; Pred. No. 0.6; 82; Mismatches CHARRAL INFORMATION
APPLICANT
APPLIC 20.2%; Score 111; CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29 PRIOR PELCATOR WINDER: TP 2001-204089
PRIOR FILING UNITS: 2001-65-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
END IN POSS ID NOS: LED9 Sequence 9552, Application US/10156761 Publication No. US20030119018A1 Streptomyces avermitilis Conservative FILE REFERENCE: 249-262 Best Local Similarity Matches 166; Conserv US-10-156-761-9552 TYPE: PRT ORGANISM: Query Match 셤 ð à 셤 ð g à g ò 셤 à 셤 δ 셤 à g ö 셤 à 셤

255 281 299 335 386

444

507 QK--DWEVN----NPQQ----LARVLKTLEGIQ------EDFNQAQSDNKAVSL-- 544

48;

Page 8

Db 346 NLNPGOCA	1::    1    1    1    1    1    1	RESULT 15 US-10-156-761-13251 US-10-156-761-13251 Sequence 13251. Application US/10156761 Publication No. US20030119018A1 GENERAL IMPORARYATION: APPLICAMY: ONURA, SANOSHI APPLICAMY: ISERIA, WINDOWNA, SANOSHI APPLICAMY: SHERA, THOSHI APPLICAMY: SHERA, THOSHI APPLICAMY: SHERA, THOSHI APPLICAMY: SHERA, THOSHI APPLICAMY: SHERA, POSHIVAL APPLICAMY: SHERA, POSHIVAL THILE OF INVENTION NOVEL POLYNUCLEOTIDES FITHE OF INVENTION NOVEL POLYNUCLEOTIDES FURE MERRERES: 249-250.	CURRENT FILLS DATE: 2001-201-201099  PRIOR APPLCATION WHERE: JF 2001-201099  PRIOR FILING DATE: 2001-05-30  PRIOR PRILICATION WHERE: JF 2001-20209  PRIOR PRILICATION WHERE: JF 2001-08-02  NUMBER OF SEQ ID NOS: 15109  SEQ ID NO 1251  LENGTH: 1205 PRIOR SPEED OF SECURITIES  GORGANISM: Streptomyces avermitilis  US-10-156-761-1351	Ouery Match  2.74; Score 110; DB 15; Length 1208;  Best Local Similarity 21.54; Precl No. 1.7;  Matches 94; Conservative 41; Hismatches 161; Indels 142; Gaps 17;  Action of Hismatches 161; Indels 142; Gaps 17;  Qy 64 SGSSTYNTHINGEKEPF-TGGIKASAGGTKREWNPMALALGIROBSGLSDPNDPD 63   1   1   1   1   1   1   1   1   1
	RESULT 14 18-2010-156-751-11828 18-20-156-751-11828 18-20-20-20-20-20-20-20-20-20-20-20-20-20-	PRYOR ADDICATION WOMER: JP 2001-272697	09   86   WIDSODWMPADYGHYGPPIRMAWHSA-GTYRIGDGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	233 VAPECPRGRAPDIALARDIETERMANDETVALIAGGHTEGKTHGAADAEKTVG

114   TYRIC DEAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

Search completed: October 7, 2003, 19:59:27 Job time : 51.241 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 7, 2003, 19:39:02 ; Scarch time 29.3425 Seconds (Without all jupments) 2441.707 Million cell updates/sec Run on:

US-09-884-889-8

1 MENHKHSGSSTYNTNTGGKC.....VKDFVKAWAKVMDLDRFDLK 745 BLOSUM62 4002 Perfect score: Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

piri:\* pir2:\* pir3:\* pir4:\* PIR\_76:\* ..... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SETERMINE

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SUMMARIES	ព	F95422	B83763	JS0520	T43873	T43874	T43878	T43880	T43881	T43877	T43882	F82584	A87626	A40662	A47685	AI0936	T45091	G91237	CSECHP	T44846	C86085	B82186	CSEBHT	T44562	AC0403	875113	T00313	A69529	871130	C98160
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•	Query Match	69.7	0.69	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	9. 79	67.2	63.6	63.5	61.1	61.0	9.09	9.09	60.5	4.09	60.4	60.1	0.09	59.5	59.0	57.8	9.98	55.8	55.1
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723	464	576	361	279	250	249	421	250	250	263	430	288	250	250	250
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2201.5	1881.5	1239	316	278.5	258	255.5	252.5	250	249	246	245.5	244.5	244	243	241
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

F95422 retalese (FC 1-11-1-6) [imported] . Sinorbimohium moliloti (stunto 1001) =================================	un page	14014	40,		
C; Species: Sinorhizobium meliloti	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TOOTTE	(scrain	1061)	mayapıasmı
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RESULT 1

Cibatts: 24-40g-2001 stequence\_revision 24-Aug-2001 steat\_change 14-Sep-2001 Cibatts: 24-Aug-2001 Fibration 14-Aug-2001 Sequence\_revision 24-Aug-2001 Cibatts 1954.25 Sebarati, M.J.: Fibrater R.F.; Jones T.F.; Jones T.F.; Jones T.F.; Denk, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K. Proc. Natl. Acad Sci. U.S.A. 99, 9833-9889, 2001. Surzycki, R.; Wells, D.H.; Yeh, K. A.Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli-Affectence number: ASSA22, MUDD:11481432

A,Accession: F954.2
A,Accession: F954.2
A,Accession: F954.2
A,Accession: F954.2
A,Betalini FP Feel Initiary
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A,Besiduse: T72 CAMP.
A,CTOSS-TEGETENCES: GB:ARDU06469; PIDN:AAKE5944.1; PID:G14524460; GSPDB:GN00165
A,CTOSS-TEGETENCES: GB:ARDU06469; PIDN:AAKE5944.1; PID:G14524460; GSPDB:GN00165
B,Gallhett, F.; Finan, T. M.; Long, S.R.; Puhller, A.; Abola, P.; Ampe, F.; Barloy-Hubl
B,Gallhett, F.; Finan, T. M.; Cookie, A.; Dayls, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
A,Title: The Composite genome of the legume symbiont Sinorhizobkum mellioli.
A,Reference number: A6039; MUD:21366234; PMID:11474104
A,TITLE: A,CONERGE: A,CO

A; Gene: SMa2379

A;Genome: plasmid C;Superfamily: catalase HPI C;Keywords: oxidoreductase

9 Indels 13; Gaps DB 2; Length 727; Ouery Match 69.7%; Score 2787.5; DB 2; Best Local Similarity 71.1%; Pred. NO. 5.3c-182; Marches 521; Conservative 72; Mismatches 127;

73 14 INTGERCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKKL ŏ

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74 DLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGGGGGGGGFAP 133 쉱 ð

134 INSWPDNANLDKARLLIMPIKQKYGRKISWADLMILIGNVALETMGFKTFGFAGGRADVW 193 ð g

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Oct 10 11:39:19 2003

C:Complex: homotetramer; two non-covalently associated iron protoheme IX groups per t C:Punction: <CAT> A;Description: as peroxidase, uses hydrogen peroxide to oxidize donor compounds produ A;Note: active with a broad spectrum of donor compounds, including larger ones which C;Superfamily: catalase HII C;Superfamily: catalase HII C;Reywords: chromoprotein; heme; homotetramer; iron; metalloprotein; oxidoreductase expression in Escherichia coli of the Baci PMID:2670897 catalase (EC 1.11.1.6) HPI - Bacillus stearothermophilus
NiAlternate names: catalase-peroxidase; hydroperoxidase I
N:Ontains: peroxidase (EC 1.11.1.7)
N:Ontains: peroxidase (EC 1.11.1.7)
C:Species Bacillus stearothermophilus
C:Dates: 30-Sep-1991 stequence\_revision 08-Nov-1996 #text\_change 03-Mar-2000
C:Accession; 30-Sep-1992 stequence\_revision 08-Nov-1996 #text\_change 03-Mar-2000
S:Northunaleamsai, S.; Aihars, S.; Miyai, K.; Suga, Y.; Yomo, T.; Negoro, S.; Urabe, S: Mitter of JIPID, July 1991
A:Reference number: 350220
A:Reference number: 350220 A; Description: as catalase, catalyzes the dismutation of two molecules of hydrogen 371 431 420 251 491 551 611 EMLVDRAOLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTK 671 WRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVKDFVK 731 HGADIITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGAGIIPDA WEPEEDVYWGAETEWL-GDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDI RETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTG HDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRY DKRGGANGARIRLAPOKDWEVNNPQQLARVLKTLEGIQEDFNOAQSDNKAVSLADLIVLA GCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAE A; Note: this sequence has been extensively revised in reference JS0520 cjeenet.dos: A; Gene perA 732 AWAKVMDLDRFDLK 745 712 AWVKVMNADRFDLK 725 C; Function: <PER> 193 182 252 242 312 421 480 672 432 492 552 612 654 594 perA 셤 ò a ò 셤 ò g ò 셤 ç g ç 셤 ò ద ö g ð Hira A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04625.1, GSPDB:GNOd A;Experimental source: strain C-125 and R:Takami H: Nakasone, K.: Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Mucleic Actid Res. 28, 4317-4331, 2000 Mucleic Actid Res. 28, 4317-4331, 2000 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A:Reference number #83569; WUID:20512582; PMID:11058132 ŝ 433 493 475 553 535 611 595 671 WRASDESDKVPEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVKDFVK 731

WSPIEGEEDVYZGADRAFFYTGEVKWSGTRYDLIFGSNSELRALAEVYAGGADREKFVKDFVK 731

WSPIEGEEDVYZGADRAFFYTGEVTRYDLIFGSHSQLARAFAFARYAGGAREKFVKDFVK 713 LDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGGGGGGRFA 132 13 NTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKK 72 C.Species Bacillus halodurans C.Fute: 0.bbc-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001 C.Accession B83000 434 PEVPQEDLIWODPIPDVSHPLVDENDIEGLKAKILESGLTVSELVSTAWASASTFRNSDK 314 ADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGAGTIPDAHD PSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRYLG RGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVLAGC AGVEKAARDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHK--VSAE **EMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNRPGQLSNDFFVNLLDLNTK** Gaps 11; DB 2; Length 735; catalase BH0906 [imported] - Bacillus halodurans (strain C-125) 69.0%; Score 2759.5; DB 2; Length 70.2%; Pred. No. 4.4e-180; 11ve: 69; Mismatches 139; Indels AWAKVMDLDRFDL 744 || |||: ||||| 714 AWTKVMNADRFDL 726 Best Local Similarity 70.2% Matches 515; Conservative C; Superfamily: catalase HPI A;Status: preliminary A;Molecule type: DNA A;Residues: 1-735 <STO> 356 464 554 536 296 BH0906 374 612 672 654 732 Query Match 73 62 133 C; Genetics 8 à 셤 ò g ò ď ò g ò g ò 8 à 셤 ö 8 g 셤 ð å ò

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Gaps 19; Length 751 Indels

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121 RGGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGF 180

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181 KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNG 

DPDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDG 120

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1 MENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPN

67.8%; Score 2714.5; DB 4; 68.7%; Pred. No. 5.3e-177; tive 75; Mismatches 139;

Best\_Local Similarity 68.7% Matches 511; Conservative

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Query Match

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300 290 360 350 420

361 DGAGAGTIPDAHDPSKSHAPFWLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKL

AWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNK 

THROMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVST

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301 SLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPK

291 GLGWISSYGKGKGSDTITSGIEGAWTPTPTQWDTSYFDMLFGYDWWLTKSPAGAWQWMAV

241 RPDPIAAARDIRETEGRAMNDEETVALIAGGHTFGKTHGAADAEKTVGREPAAAGIEEM 212 RPDFAAARDIRETFRAMMINDETVALIAGGHTFGKHGAAGF-HVQBREPAAPLEA

480 469 540 523

541 AVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRN 600

Y I K PEHKVSA EEMLVDRAQLLSLSA PEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSND 

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SEEKFVKDFVKAWAKVMDLDRFDL 744 

A.Cross-references: EMBL.AB020075; NID:g4140057; PIDN:BAA36987.1; PID:g4140058 C.Comment: For the Wild-type sequence, see PIR:380520.
C:GenetLos:
C:GenetLos:
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A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-751 <MAT>

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F.101/Active site: His (distal axial ligand) *status predicted
F.264/Findlug site: heme Lino (His) (proximal axial ligand) *status predicted
F.313/Active site: "Trp (tryptophy) radical incermediate) *status predicted
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68.7%; Pred. No. 5.1e-177;
iive 75; Mismatches 139;
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Yamamotd Y.; Miki, S.;

C;Species: synthetic A;Note: car gone engineered and expressed in Bacillus stearothermophilus C;Date: 24-Mar-2000 #sequence\_revision 24-Mar-2000 #text\_change 23-Mar-2001 C;Accession: 743874 catalase (EC 1.11.1.6) [imported] - synthetic RESULT 5

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*Matsuura, T.; Miyai, K.; Trakulnaleaamsai, S.; Yomo, T.; Shima, Y.; Miki, S.; Yamamotd
*Lalotechnia. 17, 58-61, 1999
Title: Evolutionary molecular engineering by random elongation mutagenesis.
*Reference number: 222645, MUID:99116998; PMID:9920270
                                             A/Status: translated from GB/ENBL/DDBJ
A/Alotecule type: DNA
A/Redictule type: DNA
A/Redictule (1-751 - 40472)
A/Across references: EMBL/AB020079; NID:94140065; PIDN:BNA36991.1; PID:94140066
C;Comment: For the wild-type sequence, see PIR:380520.
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1ve 75; Mismatches 139;
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ordalase (EC 1.11.1.6) [imported] - synthetic ordalase (EC 1.11.1.6) [imported] - synthetic crispectas; synthetic ch. Green engineered and expressed in Bacillus stearothermophilus (Special 24-Mar-2000) sequence_revision 24-Mar-2000 #text_change 23-Mar-2001 C.Accession: 143881 c.Accession: 143881 c.Accession: 1743881 c.Acce
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524 KVSIADLIYGGSAAVEKAARDAGFDVKPPFPGRGADATOEQTVESFRYLEPPADGFRN 893
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                                                                                                                     721 SEEKFVKDFVKAWAKVMDLDRFDL 744
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                                                                                                                                                                              catalase (EC 1.11.1.6) [Imported] - synthetic
(.)Species: synthetic
A:Note: cat gene engineered and expressed in Bacillus stearothermophilus
C:Species: A*Marz.2000 *sequence_revision 24-Narz.2000 *text_change 23-Narz.2000
C:Accession: T4380
C:Accession: T4380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.8%; Score 2714.5; DB 4; Length '68.7%; Pred. No. 5.3e-177; tvc 75; Mismatches 139; Indels
     NOEKFVRDFINAWVKVMNADRFDL 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.8%
Best Local Similarity 68.7%
Matches 511; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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702
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OY 601 YIKPEHKUSABEMLVDRAQLISISAPEMTALVGGHRVIGTNYDGSQHGVFTNKFQQQLSND 660	OY 541 AVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNFORADATAEQTDVEAFEALEPAADGFRN 600
661 FFVNLLDLATKWRASDESDKVFBGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGGAD	Db 524 KVSIADLIVLGGSRAVEKAARDAGFDVKVPFFPGRGDATQEQTDVESFAVLEPFADGFRN 583
	OY 601 YIKPBHKVSAEMLVDRAQLISISAPEMTALVGGMKVLGTNYDGSQHGVFTNKPQQLSND 660
Qy 721 SEEKFVKDEVKANAKVMDLDRFDL 744 ::   :  :  :  :  :   Db 702 NGEKFVRDFINAWVKWNADRFDL 725	
RESULT 9	721 SEEKFVKDFVKAMAKVMDLDRFDL 744
catalase (EC 1.11.1.6) [imported] • synthetic C:Species synthetic	Db 702 NQEKEVEDEINAWYKVMNADRFDL 725
A;Note: cat gene engineered and expressed in Bacillus stearothormophilus C:Note: 2-War-2000 #sequence_revision 24-Mar-2000 #text_change 23-Mar-2001 C:Acression: P43877	RESULT 10
R; Matsuura, T.; Miyal, K.; Trakulnaleaamsal, S.; Yomo, T.; Shima, Y.; Mikl, S.; Yamamotc Nat. Boltechnol, 17, 58-61, 1998	
A. Reference number: 225644; MUID:99116998; PMID:9920270	A;Note: cat gene engineered and expressed in Bacilius stearothermophilus C;Date: 24-Mar-2000 #sequence_revision 24-Mar-2000 #text_change 23-Mar-2001 C;Accession: Y4388
A:Suckus: transmared irom GB/EMBL/DDBJ A:Molecule type: NNA A:ResAdues: 1-752 <mat></mat>	R.Marsuura, T.; Miyai, K.; Trakuinaleaamsai, S.; Yomo, T.; Shima, Y.; Miki, S.; Yamam Nat.: Biotechnol. 17, 28-61, 1998 A.Title: Evolutionary molecular enchanarion by random alcomation autanomata
A:Cross-references: EMEL:AB020089; NID:g4140085; PIDN:BA37001.1; PID:g4140086 C:Comment: For the Wild-type sequence, see PIR:JS0520. C:Genefics:	A; Reference number: 22264; MUD: 916998; PMID: 9920270 A; Reference number: 22264; MUD: 9920270 A; Reference number: 22264; MUD: 9920270 A; Reference number: 22264; MUD: 9920270
A; Gene: cat C; Keywords: oxidoreductase	
8.78; Score 2714.5; DB 4; Length 752; 8.78; Pred, No. 5.3e-177;	A.Cross.references: EMBL:AB020119; NID:g4140145; PIDN:BAA37031.1; PID:g4140146 C;Comment: For the wild-type sequence, see PIR:JS0520. C;Genetics:
OV 1 MENHETSKSSTYNFRYGREEPPROCES (2) RESIDENCE 133; EUGES 13; ORDS 0;	A, were: car. C; Keywords: oxidoreductase
	8; Score 2714.5; DB 4; Length 753; 8; Pred. No. 5.3e-177;
OY 61 DPDEDYABEPKKIDLAAVKKDLAALATDSODAWPADYGHYGPPFIRMANHSAGTYRIGDG 120	Matches 511; Conservative 75; Mismatches 139; Indels 19; Gaps 6; Oy I MENHKHSGSSTYTYNTGGKCPFTGGSLKQSAGGGTKNRDWMPNMLNLGTLRQHSSLSDPN 60
121 RGGGGSGSRFAPLNSMDDNANLDKARLLLWPIKOKYGRKISWADLMILTGNVALETWGF	Db 1 MENQNRQNAAQCPFHGSVTNGSS-NRTTNKDWWPNQLNLSILHQHDRKTNPH 51
Qy 181 KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNG 240	1
Db 232 KPDFKAAARDIRETFREMGANDEETVALIAGGGTFGKAHGAGPA-THVGFEPRAAPIEAQ 290	OY 181 KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYECDRELENPLGAVQWGLIYVNPEGPWG 240 172 KTTCGACGDVWAWHEPEEDVYWGGEFFFAWA ARDVCGTREN ANIANGAT YNNANGAT ANIANGAT A
Oy 301 SIGNKTOTGIGADTITGGLEGAMTRTPOOKSNRPTENLFOYEWELTRESPACAYQMER 360 291 GLGWISSYGKGKGTTTGGLEGAMTRPPPQWDSFPRULGSTOWMLNRSPAGAWQMAN 350	241 RDP1AARDIREPGRAAMINGETVALIAGGHFGCKTHGAADAREVVGREPAAGIERH  1 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Oy 361 DGAGAGTIPDAHDSESHAPEMLTTDLALRUDPDVEKISRRYVENPDEFARAWYKL, 420  14.	Db 232 KPDFKAAARDIRETFRRAGNNDEETVALIAGGHTFGKAHGAGPA-THVGPEPEAAPIEAQ 290 301 SIGHKNTYGTGHGADTITSGLEGAATKTPTGMSNNFFENLFGYEWELTKSPAGATGWKPK 360
331 DEDENDLAFDAFDEDESKKYPTRAMITIDLALKEDPEKEKIARKFUNDEEFARANFKL. A21 HUBDAGDVIDVI OBDVINGEN TANDRIDAKONI INDRIKTARK KIAKTERIA KANTANIARI	Db 291 GLGWISSYGKGKGSDTITSGIEGAWIPTPTGWDTSYFDMLFGYDWLTKSPAGAWQWMAV 350
	DGAGAGTIPDAHDPSKSHAPFMLTTDLALRHDPDVEKISRRYENPDEFADAFAKAWYKL 
QY 401 AMASASTERNSDKRGGANGARIRLAPOKDWEVNNPOQLARVLKTLEGIOEDFNQAQSDNK 540	421

ą v	THRONGERTRYLOPEVPREDETWODP TPEVOYELT-EARLEELKAKTINSCLIV AMASASTPRUSDKRGGANGARIKLAPOKDWEVNIPOOLARVIKTLEGIOEDFNO 	QY 129 QRPAPLMSWPDNANLDKARLLMPIKQKYGKKISWADLMILTGNVALETMGFKTFGEAGG 188 145 QRPAPLMSWPDNYSLICHT
g &	470 AMASASTRANSDKRGGANGARIRLARQRDWEVNEPERLAKVLSVYEDIQRELPK 523 541 AVSLADLIVLAGGAGVERAAKDAGHEVQVPFURGRADATAEQTDVBAREALEPBAADGFRN 600	189 RADVWEREEDVYWGAETEWL-GDKRYEG
qq	524 KVSIADLIVLGGSAAVEKAARDAGFDVKVPFFPGRGDATQEQTDVESFAVLEPFADGFRN 583	205 RVDTWEPDQDVYWGRETTWLGGDVRYGAVSEGVHHPDEHRGAKEKAAKNSDSRVLENPLA
oy Qa	601 YIRPEHKVSAERHIVDRAGLISLSAPEHTALVGGHRVICTHYDGSGHGVFTNRPGGLSND 660	CY AZO AVGMOLLY VARGORANDA PLANAGULARETRAMANDENET ANLA INGERFER HEGADA 284  DD 265 AVQMOLLY VARDEGREDELASARDIRET FARMANDEET VALLAGGET GKTHGAARA 324
<i>&amp;</i> 8	661 FEVNILIDLATKARASDESDRVEEGEDFATGEVEKUSGTRVDLIFGSKISELAALARVYGCAD 720 644 FEVNILIDHAYEWVPAGGTETTRIRRYGTRVDLIFGSKISELAALARVYGCAD 720 644 FEVNILIDHAYEWVPAGGTETTRIRRYGTRVDAARVATTRICSKISTISKARAFAA	QY 285 ERYORREPAGIERAGIGARYOGOGGADATTROGLOGATTROPOGARREPALEGYE 344  1
\ & &	SEEKEVERPYKANAKVACLDRFDL 744 :::   ::  ::  :  :  :  :  :  :  :  :  :	Qy 345 WELTKEPAGAYQWKPKDGAGGTIFDAHDPSKSHAPFMLTTDLALANDPDYEKISRRYYE 404
RESULT 11 F82584		Qy 405 NEDEFADAFAKAWTKLTHRDMGPKVRYLGPEVPOEDLINGOPIPDVSHPLVDENDIEGLK 464  Db 442 HPDQSADVFRANPRANPRANPRANPROPERVERELINGOPPRVPRVADQDLLALK 501
catalase, C; Species C; Date:	omtalase/percoidase XW2222 [imported] – Xylella fastidiosa (strain 9a5c) C;Speciasi Xylella fastidiosa C;Date: 18-Aug 2000 *sesquence_arvision 20-Aug-2000 *text_change 24-Aug-2001	OY 465 AKILESGIJVSELVSTANAGASTFRNSDKROGANGARIALAPOKDWEVNNPOOLARVIKF 524  Db 502 OKISASGIJGALVSTANAGASTFROSKRGGANGGALLALAPOKOWEVNOPOQLSVYLET 561
C; ACCESS R; anonym Nature 40 A; Title:	non: F8.2344. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer 66, 131-157, 2000 at The groome sequence of the plant pathogen Xylella fastidiosa.	Oy 525 Db 562
A) Refere A) Note: A) Access A) Status	A:Reference number: A82515; MUID:20365717; PAID:10910347 A:Note: for a complete list of authors see reference number A59328 below A:Accession: F82584 A:Stetus: preliminary	OY 585 VZAFEALEPAADGFRIVIKPEHKVSAEMIVDRAQLISLSAPEMINJUGHRUGHRUD 
A; Residua A; Cross-1 A; Experin	te rype: UAA 888: 1-781 - 62HN references: GB: AED04035; GB: AED03845; NID: 99107371; PIDN: AAF65031.1; GSFDB: GN001 mental source: strain 945c	Qy 645
R;Simpso. Briones, as-Neto, submitted	J. A.J.G.; Reinhedh, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A M.R.S.; Bueno, M.R.P.; Camaryo, A.A.; Camaryo, L.E.A.; Carraro, D.M.; Carrer, F E.; Docona, C.; SI-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.	oy 705
A; Author: J.D.; Jun chado, M.	<ol> <li>Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm Stoquelir, M.L.; Remper, B.L.; Kitalian, D.P.; Kriegey, J.B.; Kitanae, E.E.; Lady A.A.; Madeira, A.M.B.N.; Modeira, H.R.F.; Marino, C.L.; Marinos, M.Y.; Martino, P.</li> </ol>	PERSIET 12
A; Author: , F.G.; I Rodrigues	A.Authors: Martins, E.M.F.; Metsukuma, A.T.; Menck, C.F.M.; Miracoa, E.C.; Miyaki, C.Y.; F.G.; Nuns, L.K.; Olivelira, M.A.; de Olivelira, M.C.; de Olivelira, R.C.; Panimeri, D.M. Rodrigues, V.; Rossa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak	NESOL 12 887626 cetalase/peroxidase [imported] - Caulobacter crescentus C.Speries: Caulobarter reserventus
A; Author: M.; Tsuh	s: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir W.M.H.; Vallada, H.; Van Silvys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z	C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C:Accession: A87626
A; Content C; Genetic	ice tummer: 0.9220 25 anotzation 85:	K.Mareman, W.C.; Fellollyum, T.V.; Faulzen, T.; Nelson, K.E.; Elsen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.R.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
C; Superfi		Proco Natl. Acad Sci. U.S.A. 99, 413-4141, 2001 A.Tille: Complete Genome Sequence of Caulobacter crescentus. A.Reference number: A87249, MUID:21173699, PMID:11259647
F; 313/B11 F; 364/Act	ryinyoving site: ins (labela and injudia) fording proficed F;315/Binding site: heme iron (His (proximal axial ligand) fording predicted F;354/Antive site: Trp (tryptophyl radical intermediate) fording predicted	A:Accession: AND AD A AND AD A A:Status: preliminary A;Molecule type: DNA
Query Match Best Local : Matches 51	Similarity 67.6%; Score 2706.5; DB 2; Length 781; 07. Conservative 86; Mismatches 131; Indels 33; Gaps 7;	A.Restudes, L./1/ CSTO> A.Restudes, L./1/ CSTO> A.CCTOSS.TG Forences: GB:AE005673; NID:gl3424687; PIDN:AAK25005.1; GSPDB:GN00148 C.Genetics: A.Gene: CG3043 A.Gene: CG3043
o,	9 SETVHTNTGRCRCPFTGGSLKGSAGGGTKNRDWHPMLNIGILRQHSSLSDPNDPDFDYAE 68 11   1   1   1   1   1   1   1   1   1	Crysuperramnity: catalase HF1 Ouery Match Ouery Match Best Local Similarity 69:5%: Pred. No. 2.1e-175;
95 10 10 10 10 10 10 10 10 10 10 10 10 10	69 EFKKLDLAAVKKDLAALWIDSODWRPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGSGS 128   :      :     :	Matches 508; Conservative 64; Mismatches 145; Indels 14; Gaps 6; Qy 15 NTGGKCPTGGSLKQSAGGGTKNROWPNMINKGILROHSSLSDPNDPDPDVAREREKKLD 74

QQ	18	18 NIAGKCPMGHGRGPANRDWWPQSLRLEGLNQHAPRSNPMGEAFDYAEAFKSLD 70	J. Bacte
ó	75	LAAVKKDLAALMIDSQDWWPADYGHYGPFFIRWAWHSAGTYRIGDGRGGGSGSGRFAPL 134	A;Title: A;Refere
g	71		A; Access A; Molecu
δy	135		A, Residu
셤	131		A;Cross- R;Zhang,
ò	195		Nature
i			A; Refere
9	Ť		A; Access
هٔ	255	FGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSL	A; Residu
ପ୍ର	250		A;Cross- C;Genet1
δ	315	DTITSGLEGAWTKTPTQWSNNFFENLFGYEWELIKSPAGAYQWKPKDGAGAGTIPDAHDP 374	A;Gene: A;Start
QQ	309		C, Comple
	į		A, Descri
ογ	375		C, Functi
QΩ	367	NYTHVPRMITSDIALREDPAYEKISRRFYENPOGFADAFARAWFKLTHRDWGPIGRYLGP 426	A; Descri
ογ	435		C; Superf
É	427	TVDXPBT.TUDDDDQVDQVDQACATANCTCXCACACACACACACACACACACACACACACACACACA	F; 108/A
3	ì	THE WELLTHOOLTH OF THE LAND AND LAND AND AND LAND AND LAND AND AND AND AND AND AND AND AND AND	F; 2/0/B1
οy	495	GGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSD	
q	487	GCANGARIKLAPQKDWAVNNPPVLAKVLAALEGVQKDFNASAGGGKKISLADLIVLGGAA 546	Ouery Best I
δý	555	GVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKP-EHKVSABEM 613	Matche
ą	547		oy
. 2	614	INDRAOL ST. SADDWITT INTERNATIONAL TOTAL STATE OF THE STA	qq
7 1			ò
gg	607	LVDRAQLIGESGPELTVLVGGLRVLGANADGSKDGVFTNRPGALSNDFFVNLLSMETTW- 665	á
Οÿ	674	ASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGGADSEEKFVKDFVKAW 733	8 8
qq	999	-SPTAANAFAGHDRKS	Š
δ	734	AKVMDLDRFDL 744	a
q	725	:	Qy
			đ
RESULT 13			ò

Carbase (EC 1.11.1.6) HPI - Mycobacterium tuberculosis (strain H37Ry)

N.Alternate names : oxtalsase-peroxidase, hydroperoxidase 1; katG catalase-peroxidase bift

N.Alternate names: oxtalsase-peroxidase, hydroperoxidase 1; katG catalase-peroxidase bift

N.Alternate names: oxtalsase-peroxidase, hydroperoxidase 1; katG catalase-peroxidase (EC 111.1.7)

C.Species: Mycobacterium tuberculosis

C. Adversasion: ANO219, ANO622, 229071, 534036

N.Cole, S. T., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Conton, R.; Davilo, R.; Parkhill, J.; Gentles, S.; Hamila, N.; Holroyd, S.; Majandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skilton, S.; Squares, S.;

N.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.;

N.Attubacs: catalase the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: pold sequence not shown; translation not shown

N.Status: nucleic acid sequence not shown; translation not shown

N.Residuse: 1-440 COD.

N.Sesiduse: 1-440 COD.

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eriol. 175, 4255-4259, 1993

:: Characterization of the KatG gene encoding a catalase-peroxidase required ence number: A40662; MUID:93308108; PMID:8320241 sion: A40662

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La type: DM. 19. CREL, 74-170, RCARNERASCRAG', 188-192, 'T', 194-207, 'DG', 210-211,'V bloss: 1.70, 'SRL', 74-170, 'RCARNERASCRAG', 188-192, 'T', 194-207, 'DG', 210-211,'V strences: 1.70, 'SRL', 74-170, 'R. 171, 'APPER, 'R. 171, 'R. 189-181, 'R. 189-18

ule type: DNA lues: 1-70,'SRL',74-80 <ZHA> -references: EMBL:X68081

1cs:

ex: homotetramer; two non-covalently associated iron protoheme IX groups per t lption: as catalase, catalyzes the dismutation of two molecules of hydrogen peron:  $\langle PER \rangle$ codon: GTG lon: <CAT>

ion: <PPEN>
iption: as peroxidase, uses hydrogen peroxide to oxidize donor compounds produ active with a broad spectrum of donor compounds, including larger ones which family: catalase HPI

ords: chromoprofelin, heme; homotetramer; iron; metalloprotein; oxidoreductase ective site; als (distal axial ligand) setatus predicted into the satial iron (His) (proximal axial ligand) setatus predicted ctive site; Trp (tryptophyl radical intermediate) \*status predicted

480; Conservative 88; Mismatches 168; Indels 10; Length 740; 63.6%; Score 2544; DB 1; 64.3%; Pred. No. 2.2e-165; Local Similarity Match

60 AAFDYAAEVATIDVDALTRDIEEVMTTSQPWWPADYGHYGPLFIRMAMHAAGTYRIHDGR 119 62 PDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGR 121 61 2 ENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTRNRDWWPNMLNLGILRQHSSLSDPND EQHPPITETTTGAASNG-CPVVGHMKYPVEGGG--NQDWWPNRLNLKVLHQNPAVADPMG

GGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFK 181 PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMS 301 LGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKD 361 TFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGK 122 182 242 239 302 a ö

AWASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQ-QIARVLKTLEGIQEDFNQAQSDN 539

540 KAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFR 599 

Fri

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Containse (Nydroperoxidase I) [imported] - Salmonella enterica subsp. enterica serovari containse (Nydroperoxidase I) [imported] - Salmonella subsp. enterica serovar Typhi Checkers in the specifies in a sequence_revision of the Typhi Checkers in the specifies in the specifies of the sequence_revision of the Typhi Checkers in the specifies of James, N. Deformation of the Typhi Checkers in the T
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                                                                                                       427
                                                                                                                                                               485
                                                                                                                                                                                             STFRNSDKRGGANGARIRLAPOKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLA 545
                                                                                                                                                                                                                                                                                                                                                                                                     665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: AL513382; PIDN: CAD09515.1; PID: 916504632; GSPDB: GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFKTFGFAGGRA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARD 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSYGTGSGKDAITSGLEVVWTPTPTKWDNSFLETLYGYEWELTKSPAGAWQFTAKDGAGA 368
                                                                                                                                                                                                                                                                                                                                                                           DLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPE 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
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                                                                             GPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVSTAWASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       666 LDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEBF
                                                   366 GTIPDAHDPSKSHAPFWLTTDLALRWDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 63.6%; Pred. No. 1.3e-158.
Matches 468; Conservative 83; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKDFVKAWAKVMDLDRFDLK 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-726 <PAR>
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C:Function: <CAT>
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                                                                                                                                                       DPFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLJFGSNSELRALAEVYGCA 719
                                                                                                                                                                                 AEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSQRFAPLNSWPDNANLDRARLLLWPIKQKYGRKISWADLMILTGNVALETMGFKTFGFA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGA 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Mortis, S.L.; Nair, J.; Rouse, D.A.
A. Gen. Microbiol. 138, 2536-2379, 1992
A.Title: The catalæse-peroxidase of Mycobacterium intracellulare; nucleotide
A:Reference number: A47685; MUID:93123988; PMID:1336034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species - Mycobacterium intracellulare
C:Date: 19-Dec-1993 #sequence_revision 08-Nov-1996 #text_change 03-Mar-2000
C:Accession: ARG
                                                                                 FGREDVWEPEE-ILWGEEEEWLGTDKRYSGERELAQPYGATTMGLIYVNPEGPEGKPDPI
IKVSFADLVVLGGCAAIEKAAKAAGHNITVPFTPGRTDASOEQTDVESFAVLEPKADGFR
                                                   NY I KPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: GB:M86741; NID:g149937; PIDN:AAA25360.1; PID:g149938
A:Note: sequence extracted from NCBI backbone (NCBIN:122093, NCBIP:122096)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             catalase (EC 1.11.1.6) HPI - Mycobacterlum intracellulare MAI Lernate names: catalase-peroxidase; hydroperoxidase I; MIBS N/Contains: peroxidase (EC 1.11.1.7)
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                                                                                                                                                                                                                                                               DSEEKFVKDFVKAWAKVMDLDRFDLK 745
                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-746 <MOR>
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371 AHDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVR 430
                                                                                                                                        489 RNSDKRGGANGARIKLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLI 548
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                                           GHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGATIPD 370
                                                       431 YLGPEVPQEDLIWQDPIPDVSHPLVD--ENDIEGLKAKILESGLTVSELVSTAWASASTF 488
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1907 THILLING HILLIAPEMTYLGGARYLGTNYGSOGOVFTORSFGYLSTDFFNILLDL
590 THILLIADAQQLILTAPEMTYLGGARYLGTNFOSGONOVFTORSFGYLSTDFFNILLDL
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Search completed: October 7, 2003, 19:46:46 Job time : 32.3425 secs

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GenCore version 5.1.6
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UG-09-884-889-8 1 MENHKHSGSSTYNTHTGGKC.....VKDFVKAWAKVMDLDRFDLK 745 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 Total number of hits satisfying chosen parameters:

830525 seqs, 258052604 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTRKNBL\_23:\*

1: ap\_arches:\*

3: ap\_barcteria:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q8ts34 methanosarc	0987s0 rhizobium 1	O939d2 burkholderi	092xq8 rhizobium m	O8pmx4 xanthomonas	O9kee6 bacillus ha	Q9s5k5 bacillus st	Q9s5r0 bacillus st	09s5n2 bacillus st	09s5k7 bacillus st	09s5q5 bacillus st	Q9s5n4 bacillus st	Q9s518 bacillus st	Q9s5p6 bacillus st	09s5q6 bacillus st	09s5q7 bacillus st
SUMMARIES	ID	Q8TS34	038750	Q939D2	Q92XGB	Q8PMX4	Q9KEE6	Q9S5R5	Q9S5R0	Q9S5N2	Q9S5K7	098505	Q9S5N4	098518	Q9S5P6	095506	098507
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	% Query Watch Length DB	736	756	748	727	756	735	743	743	744	744	745	746	748	749	750	750
	% Query Match	74.7	72.1	71.6	69.7	0.69	0.69	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8
	Score	2989.5	2884.5	2867	2787.5	2762.5	2759.5	2714.5	2714.5	2714.5	2714.5	2714.5	2714.5	2714.5	2714.5	2714.5	2714.5
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	pacifins	pacillus	bacillus	bacillus	O9s511 bacillus st	llus	bacillus	bacillus	bacillus	bacillus	bacillus	Q9s5m0 bacillus st	bacillus	bacillus	bacillus	0985n6 bacillus st	bacillus	bacillus	bacil	bacillus	Q9s516 bacillus st	bacillus	bacillus		bacillus	bacil	bacillus		bacillus
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## ALIGNMENTS

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TFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNGK 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMS 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAGTIPDAHDPSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLT 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WASASTFRNSDKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGTKNRDWWPNMLNLGILRQHSSLSDPND 61
                                               Kaneko T. Nakamura T. Saglo S. Naamizu E., Kato T. Sasamoto S.,
Hatanbe A. Ideewa K. Ishikawa A. Kawahiha K. Kimia T.,
Hatinda H. Aryokawa C. Kohata W. Matsumoto M., Matsuno A.,
Hochizulk Y. Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Complete genome structure of the nitrogen-fixing symbiotic bacterium
Hesorhizobium loil.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAFDYAEEFKSLDLDAVIXDLHALMTDSOEWWPADFGHYGPLFIRWAWHSAGTYRIADGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONRSSDMDAKTDDNSAGKCPVAHGS-----AGRTNRDWWPNQLNVQ1LHQOSSLSDPMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDF
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                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                 74; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                 7B8BAFC5DC5900AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                72.1%; Score 2884.5; DB 10
71.7%; Pred. No. 5.8e-178;
                                                                                                                                                                                                         HSSP; P00431; IBES.
InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
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PROSTES, PRODUCTOS PEROXIDASE. IN INTERPRETATION PROSTES; PEROXIDASE. IN INTERPRETATION PETOTÁLAGAS; COMPLACE POCECAME. PETOTÁLAGAS; COMPLACE POCECAME. 756 AA. 82348 MA. 788BAI
                                   MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                         EMBL; AP003010; BAB53130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 533; Conservative
                                                                                                                                                                        DNA Res. 7:331-338(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
    SEQUENCE FROM N.A. STRAIN-MAFF303099;
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                                                                                                                                       15 TSGANKQETGRDMSNRDWWPNHLKLEILHQHSSKSNPMGEDFNYAKEFKSLDLAAVKKDL 74
                                                                                                        23 TGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKKLDLAAVKKDL
                                                                                                                                                                          AALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGSGSORFAPLNSWPDNAN
                                                                                                                                                                                                                                           LDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFKTFGFAGGRADVWEPEEDVYWG
                                                                                                                                                                                                                                                             AETEWLGDKRY EGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDIRETFGRMAMND
                                                                                                                                                                                                                                                                                                                                EETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTGHGADTITSGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGYDVTVPFLPGRMDALQEQTDVVSFALLEP1ADGFRNYLKAQYPLPAEELLVDKAQLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTKWRASDESDKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVKDFVKAWAKVMDLDRF
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                                     DB 17; Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriacea; Wesorhizobium.
NCBI_TRAID-981;
                                                                    Matches 551; Conservative 62; Mismatches 108; Indels
  67A0508CD91BFA7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                 74.7%; Score 2989.5; DI
76.3%; Pred. No. 9e-185;
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  81051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-MAR-2003 (TrEMBLrel. 23,
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MLR6940.
  736 AA;
                                                    Local Similarity
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                                                                                                                                                          WEDLYNE-21236509; PubMed-11481422;
Barnett H.J. Fisher R.F., Cones T., Komp C., Abola A.P.,
Barnett H.J. Fisher R.F., Cones T., Komp C., Abola A.P.,
Gurjal M., Hong A., Bulzar L., Capala D., Gallbert F., Gouzy J.,
Gurjal M., Hong A., Bulzar L., Byman K., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M., Long S.R.;
Yeh K. C., Davis R.W., Federsplas N.A., Long S.R.;
Nucleotide sequence and predicted functions of the entire
Sinorhizobuum mellinchi Byman megaplasmid.";
Proc. Natl. Asads Sci. U.S.A. 98:988-9888 (2001).
        494 RGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVLAGC
                                                                                                                        554 AGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAEEM
                                                                                                                                                                                                                                                                                                                                                                  674 ASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVRDFVKAW
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                                     614 LVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTKWR
                                                                                                                                                                                                                                                                                                   617 LYDKAQLLTLSAPEMTYLLGGLRYLGANVGQSRHGVFTAREQALTNDFFVNLLDMGTEWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owery Match 69.7%; Score 2787.5; DB 16; Lengt Best Local Similarity 71.1%; Pred. No. 1e-11; Matches 521; Conservative 77; Mismatches 127; Indeis
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SEQUENCE 727 AA; 80292 MW; 31086D8C7AA793DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MER-2003 (TrEMBLrel, 29, Last annotation update)
Catalase/peroxidase (EC 1.11.1.6).
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Rhizobium meliloti (Sinorhizobium meliloti).
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InterPro; IPR002016; Peroxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 AKVMDLDRFDL 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 KKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDGRGGGGGGGGGRAFAPLNSWP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 VYWGAETEWL----GDKRYEGDRELENPLGAVOMGLIYVNPEGPNGKPDPIAAARDIRE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 VYWCSERIWLELSGGPNSRYSGDRQLENPLAAVQMGLIYVNPEGPDGNPDPVAAARDIRD 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVNLLDMGTEWKATSDAKDVFEGRDRKTGEVKWTGTRADLIFGSHSQLRALAEVYATADA 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 DNANLDKARLLLWPIKQKYGRKISWADIMILTGNVALETMGFKTFGFAGGRADVWEPEED 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTGHG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 TFARMAMNDEETVALIAGGHTFGKTHGAGPASN-VGAEPEAAGIEAQGLGWKSAYRTGKG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGAGTIPDAHD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHRDMGPKVRYLG 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 KCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPNDPDFDYAEEFKKLDLAAV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 KCPF----HQAAGNGTSNRDWWPNQLDLSILHRHSSLSDPMGKDFNYAQAFEKLDLAAV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loprasert S., Sallabhan R., Whangsuk W., Mongkolsuk S.;
A Burkholderla pseudomallel oxyR mutant has altered biotilm
formation, autoagoregation, extracellular protease activity, and
oxidative stress response.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
NCBI_TaxID=28450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
EMBL: AVG0244; ART74466.3; --
HSSP: P00431; IBBS.
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SEQUENCE 748 AA; 81760 MW; F59D6C8SA68SOAF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Catalase-peroxidase protein RatG.
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; Pred. No. 7.7e-177;
64; Mismatches 112;
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                                                      722 EEKFVKDFVKAWAKVMDLDRFDL 744
                                                                                       : || |||| || ||| 32 KAKPAKDEVVAWTKVMNADREDI 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002016; Peroxidase.
Pfam: PF00141: peroxidase; 1
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00436; PEROXIDASE_1: 1
PROSITE; PS00436; PEROXIDASE_2: 1.
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74.08;
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                                                                                                                                                                                                                                                                  PRELIMINARY;
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01-OCT-2002
01-MAR-2003
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Q939D2;
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343 YEWELTKSPAGAYOWKPKDGAGAGTIPDAHDPSKSHAPFMLTTDLALRMDPDYEKISRRY 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 KTLEGIQEDFNQAQSDNKAVSLADLIVLAGCAGVEKAAKDAGHEVQVPFNPGRADATAEQ 582
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Setubal J.C., Kitajima J.P.;
"Comparison of the genomes of two Xanthomones pathogens with differing
host specificatios."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGAVOMGLIYVNPEGPNGKPDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 69.04; Score 2762.5; DB 16; Length 756; Bet Local Similarity 67.34; Pered No. 4.56-170; Matches 131; Conservative 83; Mismatches 131; Indels 33;
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SEQUENCE 756 AA; 82827 MW; E7B2FDD5E979CF0F CRC64;
                                                                                                                Nature 417:459-463(2002).
MERL, AEOLI160; AAM6172.1; -.
INTERPRO: IPRO00763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                 Pfem: PF00141 percettass: 1. PRINTES PROUTES PERCETASS: 1. PRINTES PROUTES PERCETASS. 1. PROSTER; PF00045; PERCETASSE.1. 1. PROSTER; PF00045; PERCETASSE.1. 1.
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                                                                                                                                                                313
                                                                                                                                                                                                                                                                                                                          355
                                                                                                                                                                                                                                                                                                                                                                                                     LNSWPDNANLDKARRLIWPIKQKYGNRISWADLLILTGNVALESMGFKTFGFAGGRVDVW 179
                                                                                                                                                                                                                     297
                                                                                                                                                                                                                                                                         373
                                                                                                                                                                                                                                                                                                                                                                          PSKSHAPFMLTTDLALRMDPDYEKISRRYYENPDEFADAFAKAWYKLTHROMGPKVRYLG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGGANGARIRLAPOKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVLAGC 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 554 AGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHK--VSAE 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEVPQEDLIMQDPIPDVSHPLVDENDIEGLKAKILESGLIVSELVSTAWASASTFRNSDK 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTK 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEERFVKDFVK 731
                                                                                                                                                                                           EPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGL1YVNPEGPNGKPDP1AAARD1RE
                                                                                  254 TFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTGHG
                                                                                                                                                                                                                                                                     ADTITSCLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPKDGAGAGTIPDAHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
MCBL_TaxIn=92829;
NCBL_TaxIn=92829;
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on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWAKVMDLDRFDL 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KPDPIAAARDIRETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEM 300
                    611
                                                                                                                                                   1 MENHKHSGSSTYNTNTGGKCPFTGGSLKQSAGGGTKNRDWWPNMLNLGILRQHSSLSDPN 60
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                  GCAGVEKAAKDAGHEVQVPFNPGRADATAEQTDVEAFEALEPAADGFRNYIKPEHKVSAE
                                                                                          DPDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 GSAAVEKAAKEAGFDVTVPFAPGRGDATQEQTDVEGFAVLEPVSDGFRNYQKKEYSVSPE
                                                                                                                                   672 WRASDESDKVFEGRDFRTGEVKWSGTRVDLIFGSNSELRALAEVYGCADSEEKFVKDFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MENQ ------NRONAAQCPFHGSVTNQSS-NRTTNKDWWPNQLNLSILHQHDRKTNPH
                                                                         612 EMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSNDFFVNLLDLNTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE PROM N.A. Maksulra T., Miyal K., Trakulnaleaamsal S., Yomo T., Shima Y., Matsu. T., Miyal K., Trakulnaleaamsal S., Yomoo T., Shima Y., "Evolutionary molecular engineering by random elongation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
ICE 743 AA; 83874 MW; AD98CE03326DAB6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.7%; Pred. No. 5.5e-167; ive 75; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                      Firmicutes; Bacillales; Geobacillus
                                                                                                                                                                                                                                                                                                   743 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.8%; Score 2714.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000763; Bac_ctase/prase.
Interpro; IPR0007016; Peroxidase.
Interpro; IPR0007016; Peroxidase.
PRIMTS; PR00458; PEROXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGR00198; CAL_PET_HPI; 1. PROSITE; PS00435; PEROXIDASE_1; 1. PROSITE; PS00436; PEROXIDASE_2; 1.
                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                              732 AWAKVMDLDRFDLK 745
                                                                                                                                                                                                               || |||: ||||||
712 AWVKVMNADRFDLK 725
                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus stearothermophilus
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Matches 511; Conservative
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-1422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 PLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGFKTFGFAGGRADV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGRDTITSGLEGAWTANPTOWDNGFFDLLFGYEWWLTKSPAGAYQWQAVDPDEKDLAPDA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKRGGANGARIRLAPQKDWEVNNPQQLARVLKTLEGIQEDFNQAQSDNKAVSLADLIVLA 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTNNTGKCPFHHGATTSPKSSGTTNNDWPNALNLNILROHDKKSNPMGEEFDYAEEFSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 RETFGRMAMNDEETVALIAGGHTFGKTHGAADAEKYVGREPAAAGIEEMSLGWKNTYGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 WEPEEDVYWGAETEWL-GDKRYEGDRELENPLGAVQMGLIYVNPEGPNGKPDPIAAARDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                               "Complete genome sequence of the alkaliphilic bacterium Bacillus "Complete genome sequence comparison with Bacillus subtilis."; Mucleic Acids Res. 28:4317-433(2000).
Hash, AROUSIS, BAR04625.1; -1.
HSSP, PORJ.1, IAZP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 735;
                                                                                                                                                                                                                                   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui 1974] F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2759.5; DB 16; Lengt
Pred. No. 6.7e-170;
69; Mismatches 139; Indels
                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID-86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81530 MW; E93B4B5EBFA3A593 CRC64;
                                                                       Last sequence update)
Last annotation update)
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InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                TIGREAMS, TIGR00198, cat_per HPI; 1.
PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
                                                           Created)
                                                                                                                                                                            (1)
SEQUENCE FROM N.A.
SEQUENCE-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.08;
                                                         (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 70.2%;
Matches 515; Conservative 6
                              PRELIMINARY;
                                                                                                                                   Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
SEQUENCE 735 AA;
                                                                     01-0CT-2000
01-0CT-2002
Catalase.
                                                         01-OCT-2000
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OY · 1 MENHAKHSGSSTYNTNTGGKCPPTGGSLKQSAGGGTKNRDMMPMLNLGILRQHSSLSDPN 60		Qy 01 DPEDFAREE/KLAJAVKKDUALA/POSOMAPAPGRIYCEPETRAAHSAGTYRIGDG 120   11	Oy 121 RGGGGSGSQRFAPLNSWPDNANLDXARLLIMPIKQXYGRKISWADIMILTGNVALETWGF 180	112	QY 181 KTEGRAGGRADWREPERDYWGAETEWLGDKRYEGDRELENPLGAVQMGLIKVNPEGPNG 240  172 KTIGFGGRADWWRIPERDYWGSRKRALASERYSGDRELENPLAVQMGLIKVNPGPDD 231  172 KTIGFGGRADWWRIPERDYWGSRKRALASERYSGDRELENPLANDMGLIKVNPGPDG 231		Db 23.2 KPDFKAARDIKEFERRMGHNDEFTVALLAGGHFGRAHGABA-THVGFBPRAAPIEAQ 390 30.1 SLGWRKHTGHGRADITISGGLGGWWKRTPPGNEFERHEFYERRHTKFFKFRGKAGFRAFT 660	291 GLGWISSYGKGROSDTITSGIEGANTPFPTGWDYSYFDALFCYDMWLTKSPAGANOWAAV	361 DGAGACTIPDAHDPSKSHAPFMLTTDLALRNDPDYEKISRRYENPOBFADARAMYKL	DD 351 DPDEKDLAPDAEDPSKKVFTMAMTTDLALRFDFEKTARRFGUNEEFAEAFARFKL 410 OV 421 THRDMGPRURYLAPEVBORDLIMONDTDDNSHDTRGLKKKTTRGGLUNGER VGG JAG		481	Db 470 AWASASTERNSDKRGGANGARIRLAPQKDWEVNEPERLAKVLSVYEDIQRELPK 523	AVSIADLIVIAGCAGVEKAAKDAGHEVOVPENPGRADATAEQTDVEAFEALEPAADGFRN	524 KVSIADLIVLGGSAAVEKAARDAGFDVKVPFFPGRGDATOEQTDVESFAVLEPFADGFRN 601 VIEDEMEVGAPDMIVDBATI EI GABBUMATUCCUBRIT CHRINDGGALGARGA		Oy 661 FFVMLIDLATEWIASDESDKVPEGRDFWIGEWENSCIRVDLIFGSNSELRALAEWYGCAD 720  Th 644 FFVMI   1	721	DD 702 NQEKFUYDEINAWYWANDREDL 725	RESULT 9 0958HZ 1D OGGNZ 1D OG			CAT.  Bacillus stearothermophi Bacteria, Firmicutes; Ba		ngation	
Db 232 KPDPKAAARDIRETFRRGHNDEETVALIAGGHFGKAHGAGPA-THVGPEPEAAPIEAQ 290	Qy 301 SLGHKNIYGTGHGADIITSGLEGAMTKTPTGMSNNFFSNLEGYEMELKSPAGAYGMKBK 360	361 DGAGAGTIPDAHDPSKSHA	Db 351 DPDEKDLAPDAEDPSKKVPINAGTIDLALRFDPEYEKIARRFHQNPEEFARARFKL 410	THRDMGPRVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLTVSELVST	411 THRDMGPKTRYLGPEVPKE 481 AWASASTFRNSDKRGGANG	DD 470 AWASASTERNSDKRGGANGARIRLAPQKDWEVNEPERLAKVLSVYEDIQRELPK 523	Qy 541 AVSLADLIVLAGCAGVEKAAKDAGHEVQVPENEGRADATARQTDVPAFEALEPAADGFRN 600  524 N91AADLYVLAGGAAVERAARDAGFVXYPPPGRGDATQQTOVESSYNLEPPAADGFRN 593	601 YIKPEHKVSAEBKLVDRAQLISLSAPBKTALVGGKRVLGTNYDGSQHCVFTNKPGQLSND 	Db 584 YOROEYSVPPEELLYDKRAQLIGITAPEMTYLVGGLRYLGANYRDLPHGYFTDRIGYLTND 643 Ov 661 PEVNIINIANKUDAGNEGRYDFFGENEWGGRENDIN TERGENER DA ARRENGAR 110	644 FFVNILDMNYEWVPTDSGIYEIRDRKTGEVWATATRVDLIFGSROEILREYARGERVDD 644 FFVNILDMNYEWVPTDSGIYEIRDRKTGEVWATATRVDLIFGSROEILRSYARFYARDD	744	Db 702 NGEKFVBFINAWVKVHNADRFDL 725	RESULT 8	O9SSRO ID O9SSRO PRELIMINARY; PRT; 743 AA. AC O9SSRO:	01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,	DT 01-WAR-2003 (TrEMBirel. 23, Last annotation update)  B Percoxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).		(1) SEQUENCE FROM N.A.		Fr unicagenessis.  RL Mat. Blocechnol. 17:58-61(1998).  C -1- CATALYTIS ACTIVITY: 2 H (13)0(1) - 0(2) + 2 H(2)0.  CC -1- SIMILARITY: BELOXINGS TO THE PEROXIDASE FAMILY. BACTERIAL	CC PEROXIDASE/CATALASE SUBFAMILY. DR EMBL, AB0201020, BAA37032.1;	DR InterPro; TRN00765; Bac_ctase/prase. DR InterPro; TRN00705; Peroxidase.	DR PRINTS, PRO0458; PERCAIDASE; 1. DR PRINTS, PRO0458; PERCAIDASE; DR TIGRERMA; TIGRO0199; Cat_per_HP; 1. DR PROSTRE: PSOONA35; PERCAIDASE; 1.	DR PROSITE; P800436; PEROXIDASE_2; 1. KW Heme; Hydrogen peroxide; Iron, Oxidoreductase; Peroxidase. SQ SEQUENCE 743 AA; 64078 MW; ASCS422AAALCSBE CRC64;	Query Match Best Local Similarity 68.7%, Pred, No. 5.5e-16; DB 2; Length 743; Best Local Similarity 68.7%, Pred, No. 5.5e-16; Matches 511; Conservative 75: Mismatches 139; Indels 10: Gans 6.	

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THRDMGPKVRYLGPEVPQEDLIWQDPIPDVSHPLVDENDIEGLKAKILESGLIVSELVST 480
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                                                                                                                                                                                                                                                                                                                             Matsuura T., Miyai K., Trakulnaleaamsai S., Yomo T., Shima Y.,
Miki S., Yamamoto K., Urabe I.;
"Evolutionary molecular engineering by random elongation
midgenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 744;
                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Biotechnol. 17:58-61(1998).
-- CAPALYTIC. ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.
-- SIMILARITY: BELONGS TO THE PEROXIDASE PAMILY. BACTERIAL PEROXIDASE/CAPALASE SUBRAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGHPAMS: TIGMO1058. cat_per_HPI; 1.
PROSITE; PSO0435; PERCAINSE_1; 1.
PROSITE; PSO0436; PERCAINSE_2; 1.
Heme: Pydrogen percaide; Tron; Oxidoreductase; Percaidase.
PSDUDNCE 744 AA; 84000 WR; 35CEED214204FAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.8%; Score 2714.5; DB 2; Length
68.7%; Pred. No. 5.5e-167;
.ive 75; Mismatches 139; Indels
                                                                           01-MAY-2000 (TrEMBLE1. 13, Created)
MAY-2000 (TrEMBLE1. 13, Last sequence update)
01-MAR-2003 (TrEMBLE1. 23, Last annocation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
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INTERPTO: IPRO00763; BAC_CLASE/prase.
InterPto: IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00141; peroxidase; 1. PRINTS; PR00458; PEROXIDASE.
                                                                                                                                                                                                     Bacillus stearothermophilus
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                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                            744;
--- CAPALYFIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0
--- SIMILARITY: BELÖNGS TO THE PEROXIDASE PAMILY: BACTERIAL EMBL: AR020092; AR020092; ARA7004.1; ---
HESP: PO0431; 1593.
                                                                                                                                                                                                                                                                                                     Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 744 AA; 83946 MW; 34632D2BB5B109BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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68.7%; Pred. No. 5.5e-167;
                                                                                                                   Interpror IPROGNOTÉ; Bac_ctase/prase.
Interpror IPROGNOTÉ; Pac_ctase.
Prame PROGNOTÉ; PERONIDAS.
INTERPAS FROGNOTÉ PEROLIDAS.
INTERPAS FROGNOTÉS PERONIDASE.
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                  232 KPDPKAAARDIRETFRRMGMNDEETVALIAGGHTFGRAHGAGPA-THVGPEPEAAPIEAQ 290
                                                                                301 SLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPK 360
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T mitagenesis:
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SEQUENCE 746 AA; 84100 MW; 2958A4633CD63AE6 CRC64;
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68.7%; Pred. No. 5.5e-167;
ive 75; Mismatches 139; Indels
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MAY-2000 (TEBMELE) 13, Last esquence update)
01-MAR-2003 (TEBMELE) 23, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
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NCBI_TaxID-1422;
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Matches 511; Conservative
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                                                                                                                                                                               YIKPEHKVSAEEMLVDRAQLLSLSAPEMTALVGGMRVLGTNYDGSQHGVFTNKPGQLSND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 745;
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-I- SINTLARIY BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBENAHLY.
EMBL. AB020115; BAA37027.1; -
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MAY-2000 (TrEMBLE). 13, Last sequence update)
01-WAR-2003 (TrEMBLE). 23, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
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67.8%; SCORE 2714.5; DB 2;
Best Local Similarity 68.7%; Pred. No. 5.5e-167;
Conservative 75; Mismatches 139;
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                                                                                                                                                                                                                                    19;
-i- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CHALASE SUBSMILY. EMBL; AB020078; BAA36990.1; -.
                                                                                                                                                              Heme; Hydrogen peroxide; Iron, Oxidoreductase; Peroxidase.
SEQUENCE 748 AA; 84466 MW; C4BC206B26ED9CC3 CRC64;
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                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                        67.8%; Score 2714.5; DB 2;
Llarity 68.7%; Pred. No. 5.6e-167;
Conservative 75; Mismatches 139;
                                                            InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
                                                                                      Pfam: PF00141; peroxidase: 1
PRINTS: PF000458; PEROXIDASE.
TICREPAMS: TIGRN00198; cat_per_HP1; 1.
PROSITE; PS00435; PEROXIDASE_1: 1.
PROSITE; PS00436; PEROXIDASE_2: 1.
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es 511; Conserv
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                                                                                                                  RGGGGSGSQRFAPLNSWPDNANLDKARLLLWPIKQKYGRKISWADLMILTGNVALETMGF 180
                                                                                                                                  MENHKHSGSSTYNTUTGGKCPFTGGSLKQSAGGGTKNRDWWPNALNLGILRQHSSLSDPN 60
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                                                                                                                                                                          KTFGFAGGRADVWEPEEDVYWGAETEWLGDKRYEGDRELENPLGAVQMGLIYVNPEGPNG
                                                                                                                                                                                                      KTIGFGGGRVDVWHPEEDVYWGSEKEWLASERYSGDRELENPLAAVQMGLIYVNPEGPDG
                                                                                                                                                                                                                                                   SLGWKNTYGTGHGADTITSGLEGAWTKTPTQWSNNFFENLFGYEWELTKSPAGAYQWKPK
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                                                          DPDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDG
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WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
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-i- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
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Nat. Blotech
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FFVNLLDLNTKWRASDESDKVFEGRDFKTGEVKWSGTRVDLIFGSNSELRALAEVYGCAD 720
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    61 DPDFDYAEEFKKLDLAAVKKDLAALMTDSQDWWPADYGHYGPFFIRMAWHSAGTYRIGDG
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-1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
PEROXIDASE/CATALASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase,
SEQUENCE 750 AA; 84749 MW; B8E6A0ECA92BB6ED CRC64;
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68.7%; Pred. No. 5.6e-167;
ive 75; Mismatches 139; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Peroxidase/calaiase (EC 1.11.1.6) (Catalase-peroxidase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes; Bacillales; Geobacillus NCBI_TaxID=1422;
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                                                                                                                                                                                                                                                                                                                                                                                                SEEKFVKDFVKAWAKVMDLDRFDL 744
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InterPro; IPR000763; Bac_ctase/prase.
InterPro; IPR002016; Peroxidase.
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Matches 511; Conservative
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Nat. Biotech
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| Mar. Buccohnol. 17:58-61(1998).
| Mar. Buccohnol. 17:58-61(1998).
| Grandriff Garlytty: 2 H(2)(2)(2) = 0(2) + 2 H(2)0.
| STRILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL BEROXIDASE SUBFAMILY.
| PEROXIDASE SUBFAMILY.
| Mar. Bacolof, Banayonel.; | Mar. Bacchael. |
| Mar. Bacolof, Banayonel.; | Mar. Bacchael. |
| Mar. PRO11: 1819
| Mar. Bacchael. | Mar. Bacchael. | |
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                                                                                                                                                                                                                                                                                                                                                                                                                              Matsuura T., Miyai K., Trakulnaleaamsai S., Yomo T., Shima Y.,
Miki S., Yamamoto K., Urabe I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 749;
                                                                     01-WAY-2000 (TEMBLE1. 13, Created)
MAY-2000 (TEMBLE1.13, Last sequence update)
01-MAR-2003 (TEMBLE1.23, Last senottion update)
Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by random elongation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.8%; Score 2714.5; DB 2; 68.7%; Pred. No. 5.6e-167; ive 75; Mismatches 139;
                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Geobacillus
749 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *Evolutionary molecular engineering
    PRT;
                                                                                                                                                                                                                                                 Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 68.78 Matches 511; Conservative
    PRELIMINARY;
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